180925

STIC-Biotech/ChemLib

From: Chernyshev, Olga
Sent: Wednesday, March 01, 2006 9:27 AM
To: STIC-Biotech/ChemLib
Subject: 10/681,398, sequence search request

Please search SEQ ID NO: 1, 2 and 3 in regular databases only.
Thank you very much!

Olga N. Chernyshev, Ph.D.
AU 1649
REM 3C89
2-0870
mail 4C70

(STIC) MAR - 1 2006 CENTER

****
Searcher: am
Searcher Phone: 22504
Date Searcher Picked up: 3/6/06
Date completed: 3/6/06
Searcher Prep Time: 10
Online Time: 15

****
Type of Search
NA# ✓ AA#: ✓
S/L: ____ Oligomer: ____
Encode/Transl: ____
Structure #: ____ Text: ____
Inventor: ____ Litigation: ____

****
Vendors and cost where applicable
STN: ____
DIALOG: ____
QUESTEL/ORBIT: ____
LEXIS/NEXIS: ____
SEQUENCE SYSTEM: ✓
WWW/Internet: ____
Other (Specify): ____

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 12:10:20 ; Search time 9.57143 Seconds
(without alignments)
207.306 Million cell updates/sec

Title: US-10-681-398A-3
Perfect score: 151
Sequence: 1 HPKAPEPCNPKVPEPCQPKVPEPC 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	142	94.0	90	2	US-09-949-016-8088	Sequence 8088, Ap
2	140	92.7	89	2	US-09-949-016-6678	Sequence 6678, Ap
3	90	59.6	72	2	US-09-949-016-6732	Sequence 6732, Ap
4	78	51.7	161	2	US-09-123-912-114	Sequence 114, App
5	78	51.7	161	2	US-09-643-597-114	Sequence 114, App
6	78	51.7	161	2	US-09-480-884A-114	Sequence 114, App
7	78	51.7	161	2	US-09-542-615A-114	Sequence 114, App
8	78	51.7	161	2	US-09-606-421B-114	Sequence 114, App
9	78	51.7	161	2	US-09-221-107-114	Sequence 114, App
10	78	51.7	161	2	US-09-466-396A-114	Sequence 114, App
11	78	51.7	161	2	US-09-476-496A-114	Sequence 114, App
12	78	51.7	161	2	US-09-630-940B-114	Sequence 114, App
13	78	51.7	161	2	US-09-285-479-114	Sequence 114, App
14	78	51.7	161	2	US-10-007-700-114	Sequence 114, App
15	67	44.4	941	2	US-07-757-022B-14	Sequence 14, Appl
16	67	44.4	1022	2	US-07-757-022B-84	Sequence 84, Appl
17	67	44.4	1038	2	US-07-757-022B-74	Sequence 74, Appl
18	67	44.4	1049	2	US-07-757-022B-58	Sequence 58, Appl
19	67	44.4	1104	2	US-08-923-992A-4	Sequence 4, Appli
20	67	44.4	1140	2	US-07-757-022B-104	Sequence 104, App
21	67	44.4	1270	2	US-07-757-022B-44	Sequence 44, Appl
22	67	44.4	1311	2	US-07-757-022B-42	Sequence 42, Appl
23	67	44.4	1313	2	US-07-757-022B-142	Sequence 142, App
24	67	44.4	1314	2	US-07-757-022B-50	Sequence 50, Appl
25	67	44.4	1320	2	US-07-757-022B-46	Sequence 46, Appl
26	67	44.4	1320	2	US-07-757-022B-60	Sequence 60, Appl
27	67	44.4	1320	2	US-10-164-595-58	Sequence 58, Appl
28	67	44.4	1354	2	US-07-757-022B-48	Sequence 48, Appl
29	67	44.4	1361	2	US-07-757-022B-40	Sequence 40, Appl
30	67	44.4	1363	2	US-07-757-022B-52	Sequence 52, Appl
31	67	44.4	1404	2	US-07-757-022B-2	Sequence 2, Appli
32	67	44.4	1404	2	US-07-757-022B-62	Sequence 62, Appl
33	67	44.4	1404	2	US-10-164-595-78	Sequence 78, Appl
34	67	44.4	1404	2	US-09-298-970A-1	Sequence 1, Appli
35	67	44.4	1404	2	US-09-897-188-1	Sequence 1, Appli
36	67	44.4	1411	2	US-09-949-016-10827	Sequence 10827, A
37	65	43.0	984	1	US-08-242-932-2	Sequence 2, Appli
38	65	43.0	984	1	US-08-714-481-2	Sequence 2, Appli
39	65	43.0	984	4	PCT-US95-06111-2	Sequence 2, Appli
40	65	43.0	1045	2	US-09-438-185A-485	Sequence 485, App
41	65	43.0	1098	2	US-08-923-992A-8	Sequence 8, Appli
42	65	43.0	1128	2	US-08-923-992A-6	Sequence 6, Appli
43	63	41.7	846	2	US-09-858-664A-3	Sequence 3, Appli
44	63	41.7	846	2	US-10-274-978-4	Sequence 4, Appli
45	63	41.7	846	2	US-10-697-263-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-8088
; Sequence 8088, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8088
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8088

Query Match 94.0%; Score 142; DB 2; Length 90;
Best Local Similarity 91.7%; Pred. No. 1.2e-08;
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db         43 HPKVPEPCHPKVPEPCQPKVPEPC 66
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RESULT 2
US-09-949-016-6678
; Sequence 6678, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6678
;    LENGTH: 89
;    TYPE: PRT
;    ORGANISM: Human
US-09-949-016-6678

  Query Match             92.7%;  Score 140;  DB 2;  Length 89;
  Best Local Similarity   87.5%;  Pred. No. 2e-08;
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Qy          1 HPKAPEPCNPKVPEPCQPKVPEPC 24
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Db         50 HPKVPEPCQPKIPEPCQPKVPEPC 73


RESULT 3
US-09-949-016-6732
; Sequence 6732, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6732
;    LENGTH: 72
;    TYPE: PRT
;    ORGANISM: Human
;    FEATURE:
;    NAME/KEY: VARIANT
;    LOCATION: (1)...(72)
;    OTHER INFORMATION: Xaa = Any Amino Acid
US-09-949-016-6732

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  Best Local Similarity   68.0%;  Pred. No. 0.0035;
  Matches   17;  Conservative    1;  Mismatches    5;  Indels    2;  Gaps    2;

Qy          2 PKAPEPCNP-KVPEPC-QPKVPEPC 24
              || |||| | | |||| || |:||
Db         21 PKRPEPCPPLKCPEPCPPPKCPQPC 45


RESULT 4
US-09-123-912-114
; Sequence 114, Application US/09123912A
; Patent No. 6312695
; GENERAL INFORMATION:
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Wang, Tongtong
;  TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
;  FILE REFERENCE:  210121.455C1
;  CURRENT APPLICATION NUMBER: US/09/123,912A
;  CURRENT FILING DATE:  1998-07-27
;  PRIOR APPLICATION NUMBER:  09/040,802
;  PRIOR FILING DATE:  1998-03-18
;  NUMBER OF SEQ ID NOS:  114
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 114
;    LENGTH: 161
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-123-912-114

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  Best Local Similarity   60.9%;  Pred. No. 0.14;
  Matches   14;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 HPKAPEPCNPKVPEPCQPKVPEP 23
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RESULT 5
US-09-643-597-114
; Sequence 114, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Hosken, Nancy
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  McNeill, Patricia D.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.455C11
;  CURRENT APPLICATION NUMBER: US/09/643,597
;  CURRENT FILING DATE:  2000-08-21
;  NUMBER OF SEQ ID NOS:  369
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 114
;    LENGTH: 161
;    TYPE: PRT
;    ORGANISM: Homo sapien
US-09-643-597-114

  Query Match             51.7%;  Score 78;  DB 2;  Length 161;
  Best Local Similarity   60.9%;  Pred. No. 0.14;
  Matches   14;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 HPKAPEPCNPKVPEPCQPKVPEP 23
              | | |:| | |:|||   |||||
Db         42 HSKVPQPGNTKIPEPGCTKVPEP 64


RESULT 6
US-09-480-884A-114
; Sequence 114, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Hosken, Nancy A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C6
;  CURRENT APPLICATION NUMBER: US/09/480,884A
;  CURRENT FILING DATE:  2001-08-27
;  NUMBER OF SEQ ID NOS: 330
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 114
;    LENGTH: 161
;    TYPE: PRT
;    ORGANISM: Homo sapien
US-09-480-884A-114
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 12:12:18 ; Search time 3.57143 Seconds
(without alignments)
134.403 Million cell updates/sec

Title: US-10-681-398A-3
Perfect score: 151
Sequence: 1 HPKAPEPCNPKVPEPCQPKVPEPC 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	78	51.7	169	7	US-11-120-318-1	Sequence 1, Appli
3	67	44.4	941	7	US-11-169-232-14	Sequence 14, Appl
4	67	44.4	1022	7	US-11-169-232-84	Sequence 84, Appl
5	67	44.4	1038	7	US-11-169-232-74	Sequence 74, Appl
6	67	44.4	1049	7	US-11-169-232-58	Sequence 58, Appl
7	67	44.4	1140	7	US-11-169-232-104	Sequence 104, App
8	67	44.4	1270	7	US-11-169-232-44	Sequence 44, Appl
9	67	44.4	1311	7	US-11-169-232-42	Sequence 42, Appl
10	67	44.4	1313	7	US-11-169-232-142	Sequence 142, App
11	67	44.4	1314	7	US-11-169-232-50	Sequence 50, Appl
12	67	44.4	1320	7	US-11-169-232-46	Sequence 46, Appl
13	67	44.4	1320	7	US-11-169-232-60	Sequence 60, Appl
14	67	44.4	1354	7	US-11-169-232-48	Sequence 48, Appl
15	67	44.4	1361	7	US-11-169-232-40	Sequence 40, Appl
16	67	44.4	1363	7	US-11-169-232-52	Sequence 52, Appl
17	67	44.4	1404	7	US-11-169-232-2	Sequence 2, Appli
18	67	44.4	1404	7	US-11-169-232-62	Sequence 62, Appl
19	60.5	40.1	362	7	US-11-233-683-3	Sequence 3, Appli
20	60.5	40.1	377	6	US-10-999-866-37	Sequence 37, Appl
21	60.5	40.1	377	6	US-10-493-909-24	Sequence 24, Appl
22	60.5	40.1	377	7	US-11-061-821-37	Sequence 37, Appl
23	60.5	40.1	377	7	US-11-102-621-113	Sequence 113, App
24	60.5	40.1	377	7	US-11-102-621-115	Sequence 115, App
25	60.5	40.1	377	7	US-11-124-620-3	Sequence 3, Appli
26	60.5	40.1	613	7	US-11-166-994-4	Sequence 4, Appli
27	59	39.1	449	7	US-11-087-099-7707	Sequence 7707, Ap
28	56.5	37.4	237	6	US-10-330-773-9	Sequence 9, Appli
29	56	37.1	42	7	US-11-088-785-23	Sequence 23, Appl
30	56	37.1	910	7	US-11-088-785-5	Sequence 5, Appli
31	54	35.8	52	7	US-11-088-785-21	Sequence 21, Appl
32	54	35.8	54	7	US-11-088-785-22	Sequence 22, Appl
33	54	35.8	246	6	US-10-485-517-242	Sequence 242, App
34	54	35.8	350	6	US-10-485-517-209	Sequence 209, App
35	54	35.8	1410	6	US-10-821-234-1050	Sequence 1050, Ap
36	53.5	35.4	79	6	US-10-952-535A-21	Sequence 21, Appl
37	53.5	35.4	327	7	US-11-087-099-2348	Sequence 2348, Ap
38	53.5	35.4	3144	7	US-11-055-035-1	Sequence 1, Appli
39	53	35.1	186	6	US-10-508-263-111	Sequence 111, App
40	53	35.1	533	6	US-10-330-773-666	Sequence 666, App
41	53	35.1	564	7	US-11-022-289-10	Sequence 10, Appl
42	53	35.1	567	6	US-10-485-517-216	Sequence 216, App
43	53	35.1	713	6	US-10-330-773-668	Sequence 668, App
44	53	35.1	743	6	US-10-485-517-351	Sequence 351, App
45	53	35.1	877	6	US-10-485-517-200	Sequence 200, App

ALIGNMENTS

RESULT 1
US-10-623-155-114
; Sequence 114, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-114

Query Match 51.7%; Score 78; DB 6; Length 161;
Best Local Similarity 60.9%; Pred. No. 0.01;
Matches 14; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 HPKAPEPCNPKVPEPCQPKVPEP 23
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Db         42 HSKVPQPGNTKIPEPGCTKVPEP 64
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RESULT 2
US-11-120-318-1
; Sequence 1, Application US/11120318
; Publication No. US20050266497A1
; GENERAL INFORMATION:
; APPLICANT: LADENSON, JACK H.
; APPLICANT: YOUNG, PAMPEE P.
; APPLICANT: MODUR, VIJAY
; TITLE OF INVENTION: METHOD OF ASSESSING THE RISK OF ATHEROSCLEROSIS
; FILE REFERENCE: 15060-71
; CURRENT APPLICATION NUMBER: US/11/120,318
; CURRENT FILING DATE: 2005-05-02
; PRIOR APPLICATION NUMBER: 60/567,420
; PRIOR FILING DATE: 2004-04-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1

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;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-120-318-1

  Query Match            51.7%;  Score 78;  DB 7;  Length 169;
  Best Local Similarity  60.9%;  Pred. No. 0.011;
  Matches   14;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 HPKAPEPCNPKVPEPCQPKVPEP 23
              | | |:| | |:|||   |||||
Db         42 HSKVPQPGNTKIPEPGCTKVPEP 64


RESULT 3
US-11-169-232-14
; Sequence 14, Application US/11169232
; Publication No. US20060025570A1
;   GENERAL INFORMATION:
;       APPLICANT: Turner, Katherine
;                  Clark, Stephen C.
;                  Jacobs, Kenneth
;                  Hewick, Rodney M.
;                  Gesner, Thomas G.
;       TITLE OF INVENTION: Megakaryocyte Stimulating Factors
;       NUMBER OF SEQUENCES: 143
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genetics Institute, Inc.
;            STREET: 87 CambridgePark Drive
;            CITY: Cambridge
;            STATE: Massachusetts
;            COUNTRY: U.S.A.
;            ZIP: 02140
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/11/169,232
;            FILING DATE: 28-Jun-2005
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/10/124,557
;            FILING DATE: 16-Apr-2002
;            APPLICATION NUMBER: US 07/643,502
;            FILING DATE: 18-JAN-1991
;            APPLICATION NUMBER: US 07/546,114
;            FILING DATE: 29-JUN-1990
;            APPLICATION NUMBER: US 07/457,196
;            FILING DATE: 29-DEC-1989
;            APPLICATION NUMBER: US 07/390,901
;            FILING DATE: 08-AUG-1989
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Cserr, Luann
;            REGISTRATION NUMBER: 31,822
;            REFERENCE/DOCKET NUMBER: GI 5190
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617)876-1170
;            TELEFAX: (617)876-5851
;   INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 941 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-11-169-232-14

  Query Match            44.4%;  Score 67;  DB 7;  Length 941;
  Best Local Similarity  54.5%;  Pred. No. 0.83;
  Matches   12;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          2 PKAPEPCNPKVPEPCQPKVPEP 23
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Db        233 PKEPAPTTPKKPAPTTPKEPAP 254


RESULT 4
US-11-169-232-84
; Sequence 84, Application US/11169232
; Publication No. US20060025570A1
;   GENERAL INFORMATION:
;       APPLICANT: Turner, Katherine
;                  Clark, Stephen C.
;                  Jacobs, Kenneth
;                  Hewick, Rodney M.
;                  Gesner, Thomas G.
;       TITLE OF INVENTION: Megakaryocyte Stimulating Factors
;       NUMBER OF SEQUENCES: 143
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genetics Institute, Inc.
;            STREET: 87 CambridgePark Drive
;            CITY: Cambridge
;            STATE: Massachusetts
;            COUNTRY: U.S.A.
;            ZIP: 02140
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/11/169,232
;            FILING DATE: 28-Jun-2005
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/10/124,557
;            FILING DATE: 16-Apr-2002
;            APPLICATION NUMBER: US 07/643,502
;            FILING DATE: 18-JAN-1991
;            APPLICATION NUMBER: US 07/546,114
;            FILING DATE: 29-JUN-1990
;            APPLICATION NUMBER: US 07/457,196
;            FILING DATE: 29-DEC-1989
;            APPLICATION NUMBER: US 07/390,901
;            FILING DATE: 08-AUG-1989
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Cserr, Luann
;            REGISTRATION NUMBER: 31,822
;            REFERENCE/DOCKET NUMBER: GI 5190
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (617)876-1170
;            TELEFAX: (617)876-5851
;   INFORMATION FOR SEQ ID NO: 84:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1022 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-11-169-232-84

  Query Match            44.4%;  Score 67;  DB 7;  Length 1022;
  Best Local Similarity  54.5%;  Pred. No. 0.89;
  Matches   12;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          2 PKAPEPCNPKVPEPCQPKVPEP 23
              || | |  || | |  || | |
Db        314 PKEPAPTTPKKPAPTTPKEPAP 335


RESULT 5
US-11-169-232-74
; Sequence 74, Application US/11169232
; Publication No. US20060025570A1
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2006, 12:11:07 ; Search time 32.7143 Seconds
(without alignments)
306.530 Million cell updates/sec

Title: US-10-681-398A-3
Perfect score: 151
Sequence: 1 HPKAPEPCNPKVPEPCQPKVPEPC 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	151	100.0	24	5	US-10-681-398A-3	Sequence 3, Appli
2	151	100.0	144	5	US-10-681-398A-2	Sequence 2, Appli
3	140	92.7	89	4	US-10-424-599-154274	Sequence 154274,
4	139	92.1	89	5	US-10-631-467-872	Sequence 872, App
5	137	90.7	153	5	US-10-631-467-1587	Sequence 1587, Ap
6	91	60.3	72	5	US-10-287-436A-1094	Sequence 1094, Ap
7	82	54.3	125	4	US-10-425-115-201827	Sequence 201827,
8	78	51.7	161	3	US-09-735-705-114	Sequence 114, App
9	78	51.7	161	3	US-09-850-716A-114	Sequence 114, App
10	78	51.7	161	3	US-09-897-778-114	Sequence 114, App
11	78	51.7	161	3	US-09-466-396A-114	Sequence 114, App
12	78	51.7	161	4	US-10-007-700-114	Sequence 114, App
13	78	51.7	161	4	US-10-117-982-114	Sequence 114, App
14	78	51.7	161	4	US-10-313-986-114	Sequence 114, App
15	78	51.7	161	5	US-10-775-972-114	Sequence 114, App
16	78	51.7	161	5	US-10-922-124-114	Sequence 114, App
17	78	51.7	169	5	US-10-756-149-5199	Sequence 5199, Ap
18	75	49.7	110	5	US-10-883-805-3	Sequence 3, Appli
19	73	48.3	102	4	US-10-425-115-358092	Sequence 358092,
20	73	48.3	157	4	US-10-425-115-229768	Sequence 229768,
21	71	47.0	110	5	US-10-883-805-13	Sequence 13, Appl
22	69.5	46.0	233	4	US-10-767-701-46535	Sequence 46535, A
23	69	45.7	177	4	US-10-437-963-142162	Sequence 142162,
24	68	45.0	164	4	US-10-425-115-287767	Sequence 287767,
25	68	45.0	283	4	US-10-425-114-67521	Sequence 67521, A
26	67	44.4	233	4	US-10-767-701-42126	Sequence 42126, A
27	67	44.4	941	4	US-10-124-557-14	Sequence 14, Appl
28	67	44.4	1019	4	US-10-437-963-195843	Sequence 195843,
29	67	44.4	1022	4	US-10-124-557-84	Sequence 84, Appl
30	67	44.4	1038	4	US-10-124-557-74	Sequence 74, Appl
31	67	44.4	1049	4	US-10-124-557-58	Sequence 58, Appl
32	67	44.4	1104	3	US-09-797-385-4	Sequence 4, Appli
33	67	44.4	1140	4	US-10-124-557-104	Sequence 104, App
34	67	44.4	1270	4	US-10-124-557-44	Sequence 44, Appl
35	67	44.4	1311	4	US-10-124-557-42	Sequence 42, Appl
36	67	44.4	1313	4	US-10-124-557-142	Sequence 142, App
37	67	44.4	1314	4	US-10-124-557-50	Sequence 50, Appl
38	67	44.4	1320	4	US-10-124-557-46	Sequence 46, Appl
39	67	44.4	1320	4	US-10-124-557-60	Sequence 60, Appl
40	67	44.4	1320	5	US-10-717-665-58	Sequence 58, Appl
41	67	44.4	1354	4	US-10-124-557-48	Sequence 48, Appl
42	67	44.4	1361	4	US-10-124-557-40	Sequence 40, Appl
43	67	44.4	1363	4	US-10-124-557-52	Sequence 52, Appl
44	67	44.4	1404	3	US-09-802-207-30	Sequence 30, Appl
45	67	44.4	1404	3	US-09-897-188-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-681-398A-3
; Sequence 3, Application US/10681398A
; Publication No. US20050054094A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; APPLICANT: Bonilla, Iris E.
; TITLE OF INVENTION: SPRR1A AND AXONAL REGENERATION
; FILE REFERENCE: 044574-5117
; CURRENT APPLICATION NUMBER: US/10/681,398A
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US 60/285,373
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: PCT/US02/12564
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-681-398A-3

Query Match 100.0%; Score 151; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7e-09;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HPKAPEPCNPKVPEPCQPKVPEPC 24
||||||||||||||||||||||||
Db 1 HPKAPEPCNPKVPEPCQPKVPEPC 24

RESULT 2
US-10-681-398A-2
; Sequence 2, Application US/10681398A
; Publication No. US20050054094A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; APPLICANT: Bonilla, Iris E.
; TITLE OF INVENTION: SPRR1A AND AXONAL REGENERATION
; FILE REFERENCE: 044574-5117
; CURRENT APPLICATION NUMBER: US/10/681,398A
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US 60/285,373
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: PCT/US02/12564
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2

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;   LENGTH: 144
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-681-398A-2

  Query Match             100.0%;  Score 151;  DB 5;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 9e-09;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HPKAPEPCNPKVPEPCQPKVPEPC 24
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Db         65 HPKAPEPCNPKVPEPCQPKVPEPC 88


RESULT 3
US-10-424-599-154274
; Sequence 154274, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 154274
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_110330C.1.pep
US-10-424-599-154274

  Query Match             92.7%;  Score 140;  DB 4;  Length 89;
  Best Local Similarity   87.5%;  Pred. No. 8.6e-08;
  Matches   21;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 HPKAPEPCNPKVPEPCQPKVPEPC 24
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Db         50 HPKVPEPCQPKIPEPCQPKVPEPC 73


RESULT 4
US-10-631-467-872
; Sequence 872, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
;  APPLICANT: Genox Research Inc.
;  TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive p
;  TITLE OF INVENTION:  disease
;  FILE REFERENCE: 3462.1005-000
;  CURRENT APPLICATION NUMBER: US/10/631,467
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: JP 2003-077212
;  PRIOR FILING DATE: 2003-03-20
;  PRIOR APPLICATION NUMBER: JP 2002-229312
;  PRIOR FILING DATE: 2002-08-06
;  NUMBER OF SEQ ID NOS: 2086
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 872
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-631-467-872

  Query Match             92.1%;  Score 139;  DB 5;  Length 89;
  Best Local Similarity   87.5%;  Pred. No. 1.1e-07;
  Matches   21;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 HPKAPEPCNPKVPEPCQPKVPEPC 24
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Db         42 HPKVPEPCHPKVPEPCQPKLPEPC 65


RESULT 5
US-10-631-467-1587
; Sequence 1587, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
;  APPLICANT: Genox Research Inc.
;  TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive
;  TITLE OF INVENTION:  disease
;  FILE REFERENCE: 3462.1005-000
;  CURRENT APPLICATION NUMBER: US/10/631,467
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: JP 2003-077212
;  PRIOR FILING DATE: 2003-03-20
;  PRIOR APPLICATION NUMBER: JP 2002-229312
;  PRIOR FILING DATE: 2002-08-06
;  NUMBER OF SEQ ID NOS: 2086
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1587
;   LENGTH: 153
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-631-467-1587

  Query Match             90.7%;  Score 137;  DB 5;  Length 153;
  Best Local Similarity   87.5%;  Pred. No. 2.9e-07;
  Matches   21;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 HPKAPEPCNPKVPEPCQPKVPEPC 24
              ||||||||:|| |||| |||||||
Db         98 HPKAPEPCHPKAPEPCHPKVPEPC 121


RESULT 6
US-10-287-436A-1094
; Sequence 1094, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
;  APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
;  TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
;  TITLE OF INVENTION:  RHEUMATOID ARTHRITIS
;  FILE REFERENCE: 10872.514696
;  CURRENT APPLICATION NUMBER: US/10/287,436A
;  CURRENT FILING DATE:  2002-10-31
;  PRIOR APPLICATION NUMBER: US 60/336,220
;  PRIOR FILING DATE: 2001-10-31
;  NUMBER OF SEQ ID NOS: 1446
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1094
;   LENGTH: 72
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-287-436A-1094

  Query Match             60.3%;  Score 91;  DB 5;  Length 72;
  Best Local Similarity   68.0%;  Pred. No. 0.012;
  Matches   17;  Conservative    1;  Mismatches    5;  Indels    2;  Gaps    2;

Qy          2 PKAPEPC-NPKVPEPC-QPKVPEPC 24
              || ||||  || ||||  || |:||
Db         21 PKCPEPCPPPKCPEPCPPPKCPQPC 45


RESULT 7
US-10-425-115-201827
; Sequence 201827, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2006, 12:00:07 ; Search time 39.2857 Seconds
(without alignments)
268.420 Million cell updates/sec

Title: US-10-681-398A-3
Perfect score: 151
Sequence: 1 HPKAPEPCNPKVPEPCQPKVPEPC 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	151	100.0	24	6	ABB98374	Abb98374 Mouse SPR
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3	142	94.0	89	8	ADK70540	Adk70540 Respirato
4	142	94.0	89	8	ABM80143	Abm80143 Tumour-as
5	140	92.7	89	6	ABU56430	Abu56430 Lung canc
6	140	92.7	89	6	ABU56589	Abu56589 Lung canc
7	140	92.7	89	8	ADK70542	Adk70542 Respirato
8	140	92.7	89	8	ADN04648	Adn04648 Antipsori
9	140	92.7	89	8	ADN04682	Adn04682 Antipsori
10	139	92.1	89	6	ABU56433	Abu56433 Lung canc
11	139	92.1	89	6	ABU07470	Abu07470 Protein d
12	139	92.1	89	8	ADJ75620	Adj75620 Marker ge
13	139	92.1	89	8	ADN04108	Adn04108 Antipsori
14	137	90.7	153	8	ADJ76335	Adj76335 Marker ge
15	137	90.7	153	8	ADS85103	Ads85103 Mouse ato
16	134	88.7	89	9	AEA20007	Aea20007 Novel hum
17	134	88.7	152	7	ADE59751	Ade59751 Rat Prote
18	134	88.7	152	7	ADD45684	Add45684 Rat Prote
19	97	64.2	63	3	AAB38594	Aab38594 Gene 15 h
20	94	62.3	39	3	AAB38578	Aab38578 Gene 6 hu
21	91	60.3	72	6	ABU56437	Abu56437 Lung canc
22	91	60.3	72	7	ADP65153	Adp65153 Human sma
23	91	60.3	72	8	ADK70531	Adk70531 Respirato
24	91	60.3	72	8	ADN05576	Adn05576 Antipsori
25	91	60.3	76	8	ADS12207	Ads12207 Human the
26	90	59.6	72	8	ADN04978	Adn04978 Antipsori
27	79	52.3	130	4	AAB47133	Aab47133 CDIFF-14,
28	78	51.7	161	2	AAY41031	Aay41031 Human lun
29	78	51.7	161	3	AAB11316	Aab11316 Human lun
30	78	51.7	161	5	ABB74948	Abb74948 Human lun
31	78	51.7	161	5	ABP61868	Abp61868 Human lun
32	78	51.7	161	7	ADA28204	Ada28204 Human lun
33	78	51.7	161	7	ADE53409	Ade53409 Human lun
34	78	51.7	161	7	ADH36768	Adh36768 Human lun
35	78	51.7	161	8	ADK70538	Adk70538 Respirato
36	78	51.7	161	8	ADM56571	Adm56571 Human lun
37	78	51.7	161	8	ADN89615	Adn89615 Human lun
38	78	51.7	161	9	ADU98263	Adu98263 Lung tumo
39	78	51.7	161	9	AEB10071	Aeb10071 Cancer re
40	78	51.7	169	6	ABU56429	Abu56429 Lung canc
41	78	51.7	169	8	ADN05470	Adn05470 Antipsori
42	75	49.7	110	3	AAY44986	Aay44986 Human epi
43	71	47.0	73	7	ADD27804	Add27804 Human pso
44	71	47.0	73	8	ADN04331	Adn04331 Antipsori
45	71	47.0	83	8	ADS85101	Ads85101 Mouse ato

ALIGNMENTS

RESULT 1
ABB98374
ID ABB98374 standard; peptide; 24 AA.
XX
AC ABB98374;
XX
DT 04-FEB-2003 (first entry)
XX
DE Mouse SPRR1A peptide SEQ ID NO 3.
XX
KW Mouse; SPRR1A; neuron; neuroprotective; nerve growth; nerve regeneration;
KW peripheral nervous system; PNS; central nervous system; CNS.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "optional N-terminal actetyl"
FT Modified-site 24
FT /note= "optional C-terminal amide"
XX
PN WO200285116-A1.
XX
PD 31-OCT-2002.
XX
PF 22-APR-2002; 2002WO-US012564.
XX
PR 21-APR-2001; 2001US-0285373P.
XX
PA (UYYA) UNIV YALE.
XX
PI Strittmatter SM, Bonilla IE;
XX
DR WPI; 2003-093050/08.
XX
PT Inducing growth of a neuron such as peripheral nervous system neuron or a
PT central nervous system neuron of a mammal, by administering to the neuron
PT SPRR1A polypeptide or its fragment.
XX
PS Claim 3; Page 37; 72pp; English.
XX
CC The invention relates to inducing growth of a neuron, comprising
CC administering to the neuron SPRR1A polypeptide (ABB98373) encoded by a
CC nucleic acid comprising a 436 nucleotide sequence (ABV99638) or a SPRR1A
CC peptide (ABB98374). The SPRR1A polypeptide has neuroprotective activity
CC and acts as an inducer of nerve growth and regeneration. The method is
CC useful for inducing growth of a neuron such as a peripheral nervous

```
CC   system neuron or a central nervous system neuron of a mammal, preferably
CC   human. The method is also useful for inducing nerve regeneration of a
CC   damaged nerve, especially a sciatic nerve
XX
SQ   Sequence 24 AA;

  Query Match             100.0%;  Score 151;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-09;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HPKAPEPCNPKVPEPCQPKVPEPC 24
              ||||||||||||||||||||||||
Db          1 HPKAPEPCNPKVPEPCQPKVPEPC 24


RESULT 2
ABB98373
ID   ABB98373 standard; protein; 144 AA.
XX
AC   ABB98373;
XX
DT   04-FEB-2003  (first entry)
XX
DE   Mouse SPRR1A SEQ ID NO 2.
XX
KW   Mouse; SPRR1A; neuron; neuroprotective; nerve growth; nerve regeneration;
KW   peripheral nervous system; PNS; central nervous system; CNS.
XX
OS   Mus musculus.
XX
PN   WO200285116-A1.
XX
PD   31-OCT-2002.
XX
PF   22-APR-2002; 2002WO-US012564.
XX
PR   21-APR-2001; 2001US-0285373P.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Strittmatter SM,  Bonilla IE;
XX
DR   WPI; 2003-093050/08.
DR   N-PSDB; ABV99638.
XX
PT   Inducing growth of a neuron such as peripheral nervous system neuron or a
PT   central nervous system neuron of a mammal, by administering to the neuron
PT   SPRR1A polypeptide or its fragment.
XX
PS   Claim 2; Page 70-71; 72pp; English.
XX
CC   The invention relates to inducing growth of a neuron, comprising
CC   administering to the neuron SPRR1A polypeptide (ABB98373) encoded by a
CC   nucleic acid comprising a 436 nucleotide sequence (ABV99638) or a SPRR1A
CC   peptide (ABB98374). The SPRR1A polypeptide has neuroprotective activity
CC   and acts as an inducer of nerve growth and regeneration. The method is
CC   useful for inducing growth of a neuron such as a peripheral nervous
CC   system neuron or a central nervous system neuron of a mammal, preferably
CC   human. The method is also useful for inducing nerve regeneration of a
CC   damaged nerve, especially a sciatic nerve
XX
SQ   Sequence 144 AA;

  Query Match             100.0%;  Score 151;  DB 6;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-08;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 HPKAPEPCNPKVPEPCQPKVPEPC 24
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Db         65 HPKAPEPCNPKVPEPCQPKVPEPC 88


RESULT 3
ADK70540
ID   ADK70540 standard; protein; 89 AA.
XX
AC   ADK70540;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Respiratory disease differentially expressed protein #106.
XX
KW   cytostatic; respiratory; antiasthmatic; gene therapy;
KW   differential gene expression; respiratory disorder; lung cancer;
KW   chronic obstructive pulmonary disease; emphysema; asthma.
XX
OS   Homo sapiens.
XX
PN   WO2003101283-A2.
XX
PD   11-DEC-2003.
XX
PF   02-JUN-2003; 2003WO-US017409.
XX
PR   04-JUN-2002; 2002US-0386005P.
XX
PA   (INCY-) INCYTE CORP.
XX
PI   Rickert PK,  Krasnow R;
XX
DR   WPI; 2004-042945/04.
XX
PT   New combination comprising cDNAs and proteins that are differentially
PT   expressed in respiratory disorders, useful for diagnosing or treating
PT   respiratory diseases e.g. lung cancer, chronic obstructive pulmonary
PT   diseases or asthma.
XX
PS   Claim 14; SEQ ID NO 276; 343pp; English.
XX
CC   The invention relates to cDNA sequences that are differentially expressed
CC   in respiratory disorders or their complements or encoded proteins. The
CC   cDNAs and proteins are useful for diagnosing, treating or monitoring
CC   treatment of a subject with a respiratory disease including lung cancer,
CC   chronic obstructive pulmonary diseases, emphysema or asthma. The protein
CC   is also useful for screening molecules or compounds to identify at least
CC   one ligand which specifically binds the protein. It is also useful for
CC   preparing and purifying a polyclonal or monoclonal antibody. This
CC   sequence corresponds to a protein of the invention.
XX
SQ   Sequence 89 AA;

  Query Match             94.0%;  Score 142;  DB 8;  Length 89;
  Best Local Similarity   91.7%;  Pred. No. 7.1e-08;
  Matches   22;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 HPKAPEPCNPKVPEPCQPKVPEPC 24
              ||| |||| :|||||||||||||||
Db         42 HPKVPEPCHPKVPEPCQPKVPEPC 65


RESULT 4
ABM80143
ID   ABM80143 standard; protein; 89 AA.
XX
AC   ABM80143;
XX
DT   18-NOV-2004  (first entry)
XX
DE   Tumour-associated antigenic target (TAT) polypeptide PRO80646, SEQ:362.
XX
KW   Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW   tumour; diagnosis; cell proliferative disorder; breast cancer;
KW   colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW   central nervous system cancer; bladder cancer; pancreatic cancer;
KW   cervical cancer; melanoma; leukaemia; hybridisation probe;
KW   chromosome identification; chromosome mapping; gene mapping;
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OM protein - protein search, using sw model

Run on: March 6, 2006, 12:05:22 ; Search time 6.85714 Seconds
(without alignments)
336.759 Million cell updates/sec

Title: US-10-681-398A-3
Perfect score: 151
Sequence: 1 HPKAPEPCNPKVPEPCQPKVPEPC 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	142	94.0	89	2	A46709	small proline-rich
2	141	93.4	97	2	I51926	small proline-rich
3	140	92.7	89	2	I54187	small proline-rich
4	133	88.1	126	2	A46375	cornifin - rabbit
5	91	60.3	72	2	I68511	small proline-rich
6	91	60.3	72	2	S12712	small proline-rich
7	82	54.3	72	2	B27725	small proline-rich
8	70	46.4	165	2	C48232	cysteine-rich exte
9	68	45.0	491	2	T07598	proline-rich prote
10	66.5	44.0	197	2	T10081	sperm mitochondria
11	66	43.7	402	2	A40678	T-cell adhesion re
12	65	43.0	1033	2	F81595	hypothetical prote
13	65	43.0	1043	2	G86550	hypothetical prote
14	65	43.0	1043	2	G72073	hypothetical prote
15	65	43.0	1134	2	A60234	IgA Fc receptor pr
16	63.5	42.1	370	2	T49945	periaxin-like prot
17	62	41.1	160	2	D48232	cysteine-rich exte
18	62	41.1	281	2	T29150	hypothetical prote
19	62	41.1	778	2	I38487	tastin - human
20	61	40.4	161	2	E48232	cysteine-rich exte
21	61	40.4	1164	1	FCSOAG	IgA Fc receptor pr
22	60.5	40.1	90	2	A24629	Ig gamma-3 chain C
23	60.5	40.1	289	1	G3HUWI	Ig gamma-3 heavy c
24	60.5	40.1	377	2	A23511	Ig gamma-3 chain C
25	60.5	40.1	377	2	A60764	Ig gamma-3 chain C
26	60.5	40.1	1006	2	G86292	hypothetical prote
27	60.5	40.1	1494	2	T14355	protein-tyrosine-p
28	60	39.7	1037	2	B87254	translation initia
29	60	39.7	1389	2	I58157	periaxin - rat
30	59.5	39.4	266	2	T22706	hypothetical prote
31	59.5	39.4	544	2	T17547	proline-rich prote
32	59	39.1	316	2	T20497	hypothetical prote
33	59	39.1	352	2	T06482	probable cell wall
34	59	39.1	357	2	S18236	omega secalin prec
35	59	39.1	357	2	S18235	omega secalin prec
36	59	39.1	449	2	S16748	proline-rich prote
37	59	39.1	638	2	JC7753	ring finger B-box
38	58.5	38.7	289	2	T26812	hypothetical prote
39	58.5	38.7	317	2	T29960	hypothetical prote
40	58.5	38.7	753	2	JQ0532	OP protein - Kenne
41	58.5	38.7	2469	2	H36812	hypothetical prote
42	58	38.4	130	2	T49946	probable proline-r
43	58	38.4	299	2	T22705	hypothetical prote
44	58	38.4	299	2	T24833	hypothetical prote
45	58	38.4	306	2	T52340	cell wall-plasma m

ALIGNMENTS

RESULT 1
A46709
small proline-rich protein spr1 - human
N;Alternate names: keratin, small proline rich protein I
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: A46709; A27725
R;An, G.; Tesfaigzi, J.; Chuu, Y.J.; Wu, R.
J. Biol. Chem. 268, 10977-10982, 1993
A;Title: Isolation and characterization of the human spr1 gene and its regulation of exp
A;Reference number: A46709; MUID:93266543; PMID:8388378
A;Accession: A46709
A;Molecule type: DNA
A;Residues: 1-89 <AN1>
A;Cross-references: UNIPROT:P22528; UNIPARC:UPI0000127F1B; GB:M84757; NID:g338433; PIDN:
A;Note: sequence modified after extraction from NCBI backbone
A;Note: the authors translated the codon TGC for residue 65 as Lys
A;Note: sequence extracted from NCBI backbone (NCBIN:132797)
R;Kartasova, T.; van de Putte, P.
Mol. Cell. Biol. 8, 2195-2203, 1988
A;Title: Isolation, characterization, and UV-stimulated expression of two families of ge
A;Reference number: A93100; MUID:88261298; PMID:3133554
A;Accession: A27725
A;Molecule type: mRNA
A;Residues: 1-89 <KAR>
A;Cross-references: UNIPARC:UPI0000127F1B; GB:M19888; NID:g338416; PIDN:AAA36636.1; PID:
C;Superfamily: hydroxyproline-rich glycoprotein

Query Match 94.0%; Score 142; DB 2; Length 89;
Best Local Similarity 91.7%; Pred. No. 2.3e-09;
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 HPKAPEPCNPKVPEPCQPKVPEPC 24
              ||| |||| :|||||||||||||||
Db         42 HPKVPEPCHPKVPEPCQPKVPEPC 65
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RESULT 2
I51926
small proline-rich protein - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I51926
R;Tesfaigzi, J.; Wright, P.S.; Oreffo, V.; An, G.; Wu, R.; Carlson, D.M.
Am. J. Respir. Cell Mol. Biol. 9, 434-440, 1993
A;Title: A small proline-rich protein regulated by vitamin A in tracheal epithelial cell
A;Reference number: I51926; MUID:94000868; PMID:8398182
A;Accession: I51926
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-97 <TES>
A;Cross-references: UNIPROT:P35323; UNIPARC:UPI0000127F23; GB:M88166; NID:g385239; PIDN:

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C;Genetics:
A;Gene: sPRP
C;Superfamily: hydroxyproline-rich glycoprotein

  Query Match           93.4%;  Score 141;  DB 2;  Length 97;
  Best Local Similarity   91.7%;  Pred. No. 3.2e-09;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 HPKAPEPCNPKVPEPCQPKVPEPC 24
              ||| |||| ||||||||||||||||
Db         42 HPKVPEPCQPKVPEPCQPKVPEPC 65


RESULT 3
I54187
small proline-rich protein 1A - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I54187
R;Gibbs, S.; Fijneman, R.; Wiegant, J.; van Kessel, A.G.; van De Putte, P.; Backendorf,
Genomics 16, 630-637, 1993
A;Title: Molecular characterization and evolution of the SPRR family of keratinocyte dif
A;Reference number: I54187; MUID:93315153; PMID:8325635
A;Accession: I54187
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-89 <RES>
A;Cross-references: UNIPROT:P35321; UNIPARC:UPI0000127F15; GB:L05187; NID:g3327379; PIDN
C;Genetics:
A;Gene: GDB:SPRR1A
A;Cross-references: GDB:136393; OMIM:182265
A;Map position: 1q21-1q21
C;Superfamily: hydroxyproline-rich glycoprotein

  Query Match           92.7%;  Score 140;  DB 2;  Length 89;
  Best Local Similarity   87.5%;  Pred. No. 3.8e-09;
  Matches   21;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 HPKAPEPCNPKVPEPCQPKVPEPC 24
              ||| |||| ||:|||||||||||||
Db         50 HPKVPEPCQPKIPEPCQPKVPEPC 73


RESULT 4
A46375
cornifin - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46375
R;Marvin, K.W.; George, M.D.; Fujimoto, W.; Saunders, N.A.; Bernacki, S.H.; Jetten, A.M.
Proc. Natl. Acad. Sci. U.S.A. 89, 11026-11030, 1992
A;Title: Cornifin, a cross-linked envelope precursor in keratinocytes that is down-regul
A;Reference number: A46375; MUID:93066377; PMID:1438308
A;Accession: A46375
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-126 <MAR>
A;Cross-references: UNIPROT:P35324; UNIPARC:UPI0000127F17
A;Experimental source: squamous cell
A;Note: sequence extracted from NCBI backbone (NCBIN:118804, NCBIP:118807)
C;Superfamily: hydroxyproline-rich glycoprotein

  Query Match           88.1%;  Score 133;  DB 2;  Length 126;
  Best Local Similarity   91.3%;  Pred. No. 3.1e-08;
  Matches   21;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 PKAPEPCNPKVPEPCQPKVPEPC 24
              || |||| ||||||||||||||||
Db         43 PKVPEPCQPKVPEPCQPKVPEPC 65


RESULT 5
I68511
small proline-rich protein 2B - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I68511
R;Gibbs, S.; Fijneman, R.; Wiegant, J.; van Kessel, A.G.; van De Putte, P.; Backendorf,
Genomics 16, 630-637, 1993
A;Title: Molecular characterization and evolution of the SPRR family of keratinocyte di
A;Reference number: I54187; MUID:93315153; PMID:8325635
A;Accession: I68511
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-72 <RES>
A;Cross-references: UNIPROT:P35325; UNIPARC:UPI0000135D6F; GB:L05188; NID:g385226; PIDN
C;Genetics:
A;Gene: GDB:SPRR2B
A;Cross-references: GDB:136397; OMIM:182268
A;Map position: 1q21-1q21

  Query Match           60.3%;  Score 91;  DB 2;  Length 72;
  Best Local Similarity   68.0%;  Pred. No. 0.0008;
  Matches   17;  Conservative    1;  Mismatches    5;  Indels    2;  Gaps    2;

Qy          2 PKAPEPC-NPKVPEPC-QPKVPEPC 24
              || |||| || |||| || |:||
Db         21 PKCPEPCPPPKCPEPCPPPKCPQPC 45


RESULT 6
S12712
small proline-rich protein spr2-1 - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S12712
R;Gibbs, S.; Lohman, F.; Teubel, W.; van de Putte, P.; Backendorf, C.
Nucleic Acids Res. 18, 4401-4407, 1990
A;Title: Characterization of the human spr2 promoter: induction after UV irradiation or
A;Reference number: S12712; MUID:90356372; PMID:2388825
A;Accession: S12712
A;Molecule type: DNA
A;Residues: 1-72 <GIB>
A;Cross-references: UNIPROT:P35326; UNIPARC:UPI0000135D6D; EMBL:X53065; NID:g3367692; PI
C;Genetics:
A;Gene: spr2-1

  Query Match           60.3%;  Score 91;  DB 2;  Length 72;
  Best Local Similarity   68.0%;  Pred. No. 0.0008;
  Matches   17;  Conservative    1;  Mismatches    5;  Indels    2;  Gaps    2;

Qy          2 PKAPEPC-NPKVPEPC-QPKVPEPC 24
              || |||| || |||| || |:||
Db         21 PKCPEPCPPPKCPEPCPPPKCPQPC 45


RESULT 7
B27725
small proline-rich protein spr2 - human
N;Alternate names: keratin, small proline rich protein II
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C;Accession: B27725
R;Kartasova, T.; van de Putte, P.
Mol. Cell. Biol. 8, 2195-2203, 1988
A;Title: Isolation, characterization, and UV-stimulated expression of two families of ge
A;Reference number: A93100; MUID:88261298; PMID:3133554
A;Accession: B27725
A;Molecule type: mRNA
A;Residues: 1-72 <KAR>
A;Cross-references: UNIPROT:P22531; UNIPARC:UPI0000135D76; GB:M20030; NID:g338422; PIDN:

  Query Match           54.3%;  Score 82;  DB 2;  Length 72;
  Best Local Similarity   66.7%;  Pred. No. 0.0078;
  Matches   16;  Conservative    1;  Mismatches    5;  Indels    2;  Gaps    2;
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OM protein - protein search, using sw model

Run on: March 6, 2006, 12:10:20 ; Search time 57.4286 Seconds
(without alignments)
207.306 Million cell updates/sec

Title: US-10-681-398A-2
Perfect score: 880
Sequence: 1 MSSHQQKQPCTVPPQLHQQQ.....PEPCPSTVTPSPYQQKTKQK 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	424.5	48.2	161	2	US-09-123-912-114	Sequence 114, App
2	424.5	48.2	161	2	US-09-643-597-114	Sequence 114, App
3	424.5	48.2	161	2	US-09-480-884A-114	Sequence 114, App
4	424.5	48.2	161	2	US-09-542-615A-114	Sequence 114, App
5	424.5	48.2	161	2	US-09-606-421B-114	Sequence 114, App
6	424.5	48.2	161	2	US-09-221-107-114	Sequence 114, App
7	424.5	48.2	161	2	US-09-466-396A-114	Sequence 114, App
8	424.5	48.2	161	2	US-09-476-496A-114	Sequence 114, App
9	424.5	48.2	161	2	US-09-630-940B-114	Sequence 114, App
10	424.5	48.2	161	2	US-09-285-479-114	Sequence 114, App
11	424.5	48.2	161	2	US-10-007-700-114	Sequence 114, App
12	420.5	47.8	90	2	US-09-949-016-8088	Sequence 8088, Ap
13	414.5	47.1	89	2	US-09-949-016-6678	Sequence 6678, Ap
14	246	28.0	941	2	US-07-757-022B-14	Sequence 14, Appl
15	246	28.0	1022	2	US-07-757-022B-84	Sequence 84, Appl
16	246	28.0	1038	2	US-07-757-022B-74	Sequence 74, Appl
17	246	28.0	1049	2	US-07-757-022B-58	Sequence 58, Appl
18	246	28.0	1140	2	US-07-757-022B-104	Sequence 104, App
19	246	28.0	1270	2	US-07-757-022B-44	Sequence 44, Appl
20	246	28.0	1311	2	US-07-757-022B-42	Sequence 42, Appl
21	246	28.0	1313	2	US-07-757-022B-142	Sequence 142, App
22	246	28.0	1314	2	US-07-757-022B-50	Sequence 50, Appl
23	246	28.0	1320	2	US-07-757-022B-46	Sequence 46, Appl
24	246	28.0	1320	2	US-07-757-022B-60	Sequence 60, Appl
25	246	28.0	1320	2	US-10-164-595-58	Sequence 58, Appl
26	246	28.0	1354	2	US-07-757-022B-48	Sequence 48, Appl
27	246	28.0	1361	2	US-07-757-022B-40	Sequence 40, Appl
28	246	28.0	1363	2	US-07-757-022B-52	Sequence 52, Appl
29	246	28.0	1404	2	US-07-757-022B-2	Sequence 2, Appli
30	246	28.0	1404	2	US-07-757-022B-62	Sequence 62, Appl
31	246	28.0	1404	2	US-10-164-595-78	Sequence 78, Appl
32	246	28.0	1404	2	US-09-298-970A-1	Sequence 1, Appli
33	246	28.0	1404	2	US-09-897-188-1	Sequence 1, Appli
34	246	28.0	1411	2	US-09-949-016-10827	Sequence 10827, A
35	211.5	24.0	439	2	US-10-300-819B-21	Sequence 21, Appl
36	209.5	23.8	207	1	US-07-836-642-2	Sequence 2, Appli
37	209.5	23.8	207	1	US-08-169-563-2	Sequence 2, Appli
38	209.5	23.8	207	1	US-08-403-379A-6	Sequence 6, Appli
39	209.5	23.8	207	1	US-08-557-309B-50	Sequence 50, Appl
40	209.5	23.8	207	1	US-08-929-414-6	Sequence 6, Appli
41	209.5	23.8	207	2	US-08-834-306-50	Sequence 50, Appl
42	209.5	23.8	207	2	US-08-993-674A-50	Sequence 50, Appl
43	209.5	23.8	207	2	US-09-256-976-50	Sequence 50, Appl
44	207	23.5	174	2	US-09-248-796A-25211	Sequence 25211, A
45	198	22.5	826	1	US-07-638-431-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-123-912-114
; Sequence 114, Application US/09123912A
; Patent No. 6312695
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.455C1
; CURRENT APPLICATION NUMBER: US/09/123,912A
; CURRENT FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: 09/040,802
; PRIOR FILING DATE: 1998-03-18
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 114
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-123-912-114

Query Match 48.2%; Score 424.5; DB 2; Length 161;
Best Local Similarity 57.8%; Pred. No. 1.6e-27;
Matches 93; Conservative 6; Mismatches 45; Indels 17; Gaps 3;

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Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCH-PVPEPCNPKGPEPCHPK 59
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Db          1 MSSYQQKQTFTPPPQLQQQQVKQPSQPPPQEIFVPTTKEPCHSKVPQPGNTKIPEPGCTK 60

Qy         60 APEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEP-------------CQP 106
                |||   | |||   |||||   |||||   |||||   |||||             :|
Db         61 VPEPGCTKVPEPGCTKVPEPGCTKVPEPGCTKVPEPGYTKVPEPGSIKVPDQGFIKFPEP 120

Qy        107 ---KAPEPCHPKAPEPCHPVVPEPCPSTVTPSPYQQKTKQK 144
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Db        121 GAIKVPEQGGYTKVPVPGYTKVPEPCPSTVTPGPAQQKTKQK 161
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RESULT 2
US-09-643-597-114
; Sequence 114, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.

```
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  McNeill, Patricia D.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.455C11
;  CURRENT APPLICATION NUMBER: US/09/643,597
;  CURRENT FILING DATE:  2000-08-21
;  NUMBER OF SEQ ID NOS:  369
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 114
;   LENGTH: 161
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-643-597-114

  Query Match             48.2%;  Score 424.5;  DB 2;  Length 161;
  Best Local Similarity   57.8%;  Pred. No. 1.6e-27;
  Matches   93;  Conservative    6;  Mismatches   45;  Indels   17;  Gaps    3;

Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCH-PVPEPCNPKGPEPCHPK 59
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Qy         60 APEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEP------------CQP 106
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Qy        107 ---KAPEPCHPKAPEPCHPVVPEPCPSTVTPSPYQQKTKQK 144
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Db        121 GAIKVPEQGYTKVPVPGYTKVPEPCPSTVTPGPAQQKTKQK 161


RESULT 3
US-09-480-884A-114
; Sequence 114, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Hosken, Nancy A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C6
;  CURRENT APPLICATION NUMBER: US/09/480,884A
;  CURRENT FILING DATE:  2001-08-27
;  NUMBER OF SEQ ID NOS: 330
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 114
;   LENGTH: 161
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-480-884A-114

  Query Match             48.2%;  Score 424.5;  DB 2;  Length 161;
  Best Local Similarity   57.8%;  Pred. No. 1.6e-27;
  Matches   93;  Conservative    6;  Mismatches   45;  Indels   17;  Gaps    3;

Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCH-PVPEPCNPKGPEPCHPK 59
              |||:||||  | |||| ||||||| ||||||   | ||:|||  ||:| | | |||   |
Db          1 MSSYQQKQTFTPPPQLQQQQVKQPSQPPPQEIFVPTTKEPCHSKVPQPGNTKIPEPGCTK 60

Qy         60 APEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEP------------CQP 106
              |||   | |||   |||||  |||||  |||||  |||||              :|
Db         61 VPEPGCTKVPEPGCTKVPEPGCTKVPEPGCTKVPEPGYTKVPEPGSIKVPDQGFIKFPEP 120

Qy        107 ---KAPEPCHPKAPEPCHPVVPEPCPSTVTPSPYQQKTKQK 144
                | ||  : | | | :  ||||||||||| | |||||||
Db        121 GAIKVPEQGYTKVPVPGYTKVPEPCPSTVTPGPAQQKTKQK 161


RESULT 4
US-09-542-615A-114
; Sequence 114, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Hosken, Nancy A.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION:  COMPOUNDS AND METHODS FOR THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.455C8
;  CURRENT APPLICATION NUMBER: US/09/542,615A
;  CURRENT FILING DATE:  2000-04-14
;  NUMBER OF SEQ ID NOS:  350
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 114
;   LENGTH: 161
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-542-615A-114

  Query Match             48.2%;  Score 424.5;  DB 2;  Length 161;
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  Matches   93;  Conservative    6;  Mismatches   45;  Indels   17;  Gaps    3;

Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCH-PVPEPCNPKGPEPCHPK 59
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Qy        107 ---KAPEPCHPKAPEPCHPVVPEPCPSTVTPSPYQQKTKQK 144
                | ||  : | | | :  ||||||||||| | |||||||
Db        121 GAIKVPEQGYTKVPVPGYTKVPEPCPSTVTPGPAQQKTKQK 161


RESULT 5
US-09-606-421B-114
; Sequence 114, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Hosken, Nancy
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C9
;  CURRENT APPLICATION NUMBER: US/09/606,421B
;  CURRENT FILING DATE:  2000-06-28
;  NUMBER OF SEQ ID NOS: 358
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 114
;   LENGTH: 161
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-606-421B-114

  Query Match             48.2%;  Score 424.5;  DB 2;  Length 161;
  Best Local Similarity   57.8%;  Pred. No. 1.6e-27;
  Matches   93;  Conservative    6;  Mismatches   45;  Indels   17;  Gaps    3;
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2006, 12:12:18 ; Search time 21.4286 Seconds
(without alignments)
134.403 Million cell updates/sec

Title: US-10-681-398A-2
Perfect score: 880
Sequence: 1 MSSHQQKQPCTVPPQLHQQQ.....PEPCPSTVTPSPYQQKTKQK 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	424.5	48.2	161	6	US-10-623-155-114	Sequence 114, App
2	423.5	48.1	169	7	US-11-120-318-1	Sequence 1, Appli
3	246	28.0	941	7	US-11-169-232-14	Sequence 14, Appl
4	246	28.0	1022	7	US-11-169-232-84	Sequence 84, Appl
5	246	28.0	1038	7	US-11-169-232-74	Sequence 74, Appl
6	246	28.0	1049	7	US-11-169-232-58	Sequence 58, Appl
7	246	28.0	1140	7	US-11-169-232-104	Sequence 104, App
8	246	28.0	1270	7	US-11-169-232-44	Sequence 44, Appl
9	246	28.0	1311	7	US-11-169-232-42	Sequence 42, Appl
10	246	28.0	1313	7	US-11-169-232-142	Sequence 142, App
11	246	28.0	1314	7	US-11-169-232-50	Sequence 50, Appl
12	246	28.0	1320	7	US-11-169-232-46	Sequence 46, Appl
13	246	28.0	1320	7	US-11-169-232-60	Sequence 60, Appl
14	246	28.0	1354	7	US-11-169-232-48	Sequence 48, Appl
15	246	28.0	1361	7	US-11-169-232-40	Sequence 40, Appl
16	246	28.0	1363	7	US-11-169-232-52	Sequence 52, Appl
17	246	28.0	1404	7	US-11-169-232-2	Sequence 2, Appli
18	246	28.0	1404	7	US-11-169-232-62	Sequence 62, Appl
19	199	22.6	449	7	US-11-087-099-7707	Sequence 7707, Ap
20	188	21.4	1000	7	US-11-036-256-95	Sequence 95, Appl
21	188	21.4	1001	7	US-11-036-256-5	Sequence 5, Appli
22	188	21.4	1001	7	US-11-036-256-96	Sequence 96, Appl
23	167	19.0	101	7	US-11-036-256-158	Sequence 158, App
24	167	19.0	101	7	US-11-036-256-159	Sequence 159, App
25	167	19.0	186	6	US-10-508-263-111	Sequence 111, App
26	163	18.5	160	6	US-10-508-263-110	Sequence 110, App
27	156.5	17.8	411	7	US-11-036-256-89	Sequence 89, Appl
28	153	17.4	346	7	US-11-036-256-33	Sequence 33, Appl
29	149	16.9	183	7	US-11-036-256-21	Sequence 21, Appl
30	149	16.9	228	7	US-11-036-256-31	Sequence 31, Appl
31	148	16.8	200	7	US-11-036-256-27	Sequence 27, Appl
32	146.5	16.6	432	7	US-11-140-417-4	Sequence 4, Appli
33	141	16.0	1562	7	US-11-052-554A-211	Sequence 211, App
34	140	15.9	2551	7	US-11-052-554A-368	Sequence 368, App
35	134	15.2	565	6	US-10-055-877-228	Sequence 228, App
36	134	15.2	1560	7	US-11-059-982-1	Sequence 1, Appli
37	131	14.9	548	7	US-11-052-554A-324	Sequence 324, App
38	129.5	14.7	395	6	US-10-330-773-661	Sequence 661, App
39	129.5	14.7	406	7	US-11-107-028-7	Sequence 7, Appli
40	129.5	14.7	559	6	US-10-793-626-1376	Sequence 1376, Ap
41	129.5	14.7	797	6	US-10-330-773-663	Sequence 663, App
42	127.5	14.5	377	6	US-10-999-866-37	Sequence 37, Appl
43	127.5	14.5	377	6	US-10-493-909-24	Sequence 24, Appl
44	127.5	14.5	377	7	US-11-061-821-37	Sequence 37, Appl
45	127.5	14.5	377	7	US-11-102-621-113	Sequence 113, App

ALIGNMENTS

RESULT 1
US-10-623-155-114
; Sequence 114, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-114

Query Match 48.2%; Score 424.5; DB 6; Length 161;
Best Local Similarity 57.8%; Pred. No. 6.1e-28;
Matches 93; Conservative 6; Mismatches 45; Indels 17; Gaps 3;

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Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCH-PVPEPCNPKGPEPCHPK 59
              |||:||||  | |||| ||||||| ||||||   | ||:|||  ||:| | | |||   |
Db          1 MSSYQQKQTFTPPPQLQQQQVKQPSQPPPQEIFVPTTKEPCHSKVPQPGNTKIPEPGCTK 60

Qy         60 APEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEP------------CQP 106
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Db         61 VPEPGCTKVPEPGCTKVPEPGCTKVPEPGCTKVPEPGYTKVPEPGSIKVPDQGFIKFPEP 120

Qy        107 ---KAPEPCHPKAPEPCHPVVPEPCPSTVTPSPYQQKTKQK 144
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Db        121 GAIKVPEQGYTKVPVPGYTKVPEPCPSTVTPGPAQQKTKQK 161
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RESULT 2
US-11-120-318-1
; Sequence 1, Application US/11120318
; Publication No. US20050266497A1
; GENERAL INFORMATION:
; APPLICANT: LADENSON, JACK H.
; APPLICANT: YOUNG, PAMPEE P.
; APPLICANT: MODUR, VIJAY
; TITLE OF INVENTION: METHOD OF ASSESSING THE RISK OF ATHEROSCLEROSIS

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;  FILE REFERENCE: 15060-71
;  CURRENT APPLICATION NUMBER: US/11/120,318
;  CURRENT FILING DATE:  2005-05-02
;  PRIOR APPLICATION NUMBER: 60/567,420
;  PRIOR FILING DATE: 2004-04-30
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
;   LENGTH: 169
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-120-318-1

  Query Match             48.1%;  Score 423.5;  DB 7;  Length 169;
  Best Local Similarity   54.4%;  Pred. No. 7.6e-28;
  Matches   92;  Conservative    6;  Mismatches   46;  Indels   25;  Gaps    2;

Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCH-PVPEPCNPKGPEPCHPK 59
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Db          1 MSSYQQKQTFTPPPQLQQQQVKQPSQPPPQEIFVPTTKEPCHSKVPQPGNTKIPEPGCTK 60

Qy         60 APEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEPCQPKAPEP-------- 111
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Qy        112 ----------------CHPKAPEPCHPVVPEPCPSTVTPSPYQQKTKQK 144
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Db        121 GFIKFPEPGAIKVPEQGYTKVPVPGYTKLPEPCPSTVTPGPAQQKTKQK 169


RESULT 3
US-11-169-232-14
; Sequence 14, Application US/11169232
; Publication No. US20060025570A1
;   GENERAL INFORMATION:
;        APPLICANT: Turner, Katherine
;                   Clark, Stephen C.
;                   Jacobs, Kenneth
;                   Hewick, Rodney M.
;                   Gesner, Thomas G.
;        TITLE OF INVENTION: Megakaryocyte Stimulating Factors
;        NUMBER OF SEQUENCES: 143
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genetics Institute, Inc.
;             STREET: 87 CambridgePark Drive
;             CITY: Cambridge
;             STATE: Massachusetts
;             COUNTRY: U.S.A.
;             ZIP: 02140
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/169,232
;             FILING DATE: 28-Jun-2005
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/10/124,557
;             FILING DATE: 16-Apr-2002
;             APPLICATION NUMBER: US 07/643,502
;             FILING DATE: 18-JAN-1991
;             APPLICATION NUMBER: US 07/546,114
;             FILING DATE: 29-JUN-1990
;             APPLICATION NUMBER: US 07/457,196
;             FILING DATE: 29-DEC-1989
;             APPLICATION NUMBER: US 07/390,901
;             FILING DATE: 08-AUG-1989
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Cserr, Luann
;             REGISTRATION NUMBER: 31,822
;             REFERENCE/DOCKET NUMBER: GI 5190
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617)876-1170
;             TELEFAX: (617)876-5851
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 941 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-11-169-232-14

  Query Match             28.0%;  Score 246;  DB 7;  Length 941;
  Best Local Similarity   40.9%;  Pred. No. 4.5e-13;
  Matches   56;  Conservative    6;  Mismatches   69;  Indels    6;  Gaps    4;

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Qy         65 HPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEPCQPKAPEPCHPKAPEPCHPVV 124
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Db        305 KEPAPTTTKEPSPTTPK 321


RESULT 4
US-11-169-232-84
; Sequence 84, Application US/11169232
; Publication No. US20060025570A1
;   GENERAL INFORMATION:
;        APPLICANT: Turner, Katherine
;                   Clark, Stephen C.
;                   Jacobs, Kenneth
;                   Hewick, Rodney M.
;                   Gesner, Thomas G.
;        TITLE OF INVENTION: Megakaryocyte Stimulating Factors
;        NUMBER OF SEQUENCES: 143
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genetics Institute, Inc.
;             STREET: 87 CambridgePark Drive
;             CITY: Cambridge
;             STATE: Massachusetts
;             COUNTRY: U.S.A.
;             ZIP: 02140
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/169,232
;             FILING DATE: 28-Jun-2005
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
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;             FILING DATE: 16-Apr-2002
;             APPLICATION NUMBER: US 07/643,502
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;             FILING DATE: 29-DEC-1989
;             APPLICATION NUMBER: US 07/390,901
;             FILING DATE: 08-AUG-1989
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Cserr, Luann
;             REGISTRATION NUMBER: 31,822
;             REFERENCE/DOCKET NUMBER: GI 5190
;        TELECOMMUNICATION INFORMATION:
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GenCore version 5.1.7
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306.530 Million cell updates/sec

Title: US-10-681-398A-2
Perfect score: 880
Sequence: 1 MSSHQQKQPCTVPPQLHQQQ.....PEPCPSTVTPSPYQQKTKQK 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	880	100.0	144	5	US-10-681-398A-2	Sequence 2, Appli
2	712.5	81.0	153	5	US-10-631-467-1587	Sequence 1587, Ap
3	424.5	48.2	161	3	US-09-735-705-114	Sequence 114, App
4	424.5	48.2	161	3	US-09-850-716A-114	Sequence 114, App
5	424.5	48.2	161	3	US-09-897-778-114	Sequence 114, App
6	424.5	48.2	161	3	US-09-466-396A-114	Sequence 114, App
7	424.5	48.2	161	4	US-10-007-700-114	Sequence 114, App
8	424.5	48.2	161	4	US-10-117-982-114	Sequence 114, App
9	424.5	48.2	161	4	US-10-313-986-114	Sequence 114, App
10	424.5	48.2	161	5	US-10-775-972-114	Sequence 114, App
11	424.5	48.2	161	5	US-10-922-124-114	Sequence 114, App
12	423.5	48.1	169	5	US-10-756-149-5199	Sequence 5199, Ap
13	417.5	47.4	89	5	US-10-631-467-872	Sequence 872, App
14	414.5	47.1	89	4	US-10-424-599-154274	Sequence 154274,
15	317.5	36.1	125	4	US-10-425-115-201827	Sequence 201827,
16	246	28.0	941	4	US-10-124-557-14	Sequence 14, Appl
17	246	28.0	1022	4	US-10-124-557-84	Sequence 84, Appl
18	246	28.0	1038	4	US-10-124-557-74	Sequence 74, Appl
19	246	28.0	1049	4	US-10-124-557-58	Sequence 58, Appl
20	246	28.0	1140	4	US-10-124-557-104	Sequence 104, App
21	246	28.0	1270	4	US-10-124-557-44	Sequence 44, Appl
22	246	28.0	1311	4	US-10-124-557-42	Sequence 42, Appl
23	246	28.0	1313	4	US-10-124-557-142	Sequence 142, App
24	246	28.0	1314	4	US-10-124-557-50	Sequence 50, Appl
25	246	28.0	1320	4	US-10-124-557-46	Sequence 46, Appl
26	246	28.0	1320	4	US-10-124-557-60	Sequence 60, Appl
27	246	28.0	1320	5	US-10-717-665-58	Sequence 58, Appl
28	246	28.0	1354	4	US-10-124-557-48	Sequence 48, Appl
29	246	28.0	1361	4	US-10-124-557-40	Sequence 40, Appl
30	246	28.0	1363	4	US-10-124-557-52	Sequence 52, Appl
31	246	28.0	1404	3	US-09-802-207-30	Sequence 30, Appl
32	246	28.0	1404	3	US-09-897-188-1	Sequence 1, Appli
33	246	28.0	1404	4	US-10-124-557-2	Sequence 2, Appli
34	246	28.0	1404	4	US-10-124-557-62	Sequence 62, Appl
35	246	28.0	1404	5	US-10-858-595-1	Sequence 1, Appli
36	246	28.0	1404	5	US-10-868-577A-55	Sequence 55, Appl
37	246	28.0	1404	5	US-10-717-665-78	Sequence 78, Appl
38	228	25.9	435	4	US-10-437-963-112015	Sequence 112015,
39	217	24.7	251	4	US-10-425-115-207693	Sequence 207693,
40	217	24.7	329	4	US-10-437-963-197333	Sequence 197333,
41	215	24.4	217	4	US-10-437-963-181576	Sequence 181576,
42	212.5	24.1	195	4	US-10-437-963-106240	Sequence 106240,
43	212	24.1	285	4	US-10-437-963-189482	Sequence 189482,
44	211.5	24.0	431	4	US-10-437-963-204963	Sequence 204963,
45	211	24.0	159	4	US-10-425-115-320315	Sequence 320315,

ALIGNMENTS

RESULT 1
US-10-681-398A-2
; Sequence 2, Application US/10681398A
; Publication No. US20050054094A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; APPLICANT: Bonilla, Iris E.
; TITLE OF INVENTION: SPRR1A AND AXONAL REGENERATION
; FILE REFERENCE: 044574-5117
; CURRENT APPLICATION NUMBER: US/10/681,398A
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US 60/285,373
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: PCT/US02/12564
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-681-398A-2

Query Match 100.0%; Score 880; DB 5; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.3e-56;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCHPVPEPCNPKGPEPCHPKA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCHPVPEPCNPKGPEPCHPKA 60

Qy         61 PEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEPCQPKAPEPCHPKAPEPC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEPCQPKAPEPCHPKAPEPC 120

Qy        121 HPVVPEPCPSTVTPSPYQQKTKQK 144
              ||||||||||||||||||||||||
Db        121 HPVVPEPCPSTVTPSPYQQKTKQK 144
```

RESULT 2
US-10-631-467-1587
; Sequence 1587, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive
; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467

```
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: JP 2003-077212
;  PRIOR FILING DATE: 2003-03-20
;  PRIOR APPLICATION NUMBER: JP 2002-229312
;  PRIOR FILING DATE: 2002-08-06
;  NUMBER OF SEQ ID NOS: 2086
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1587
;   LENGTH: 153
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-631-467-1587

  Query Match           81.0%;  Score 712.5;  DB 5;  Length 153;
  Best Local Similarity  76.5%;  Pred. No. 1.9e-44;
  Matches  117;  Conservative    7;  Mismatches   20;  Indels    9;  Gaps    2;

Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTK--------DPCHP-VPEPCNPK 51
              ||||||||||| ||||||:|||||||||||| |||  : |        :||||  ||||:||
Db          1 MSSHQQKQPCTAPPQLHEQQVKQPCQPPPPEPCVSQVKTPCDTKVPEPCHPKAPEPCHPK 60

Qy         52 GPEPCHPKAPEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEPCQPKAPEP 111
              ||||||||||||||||||||:|| |||| || |||| || ||||:|| |||| || |||
Db         61 APEPCHPKAPEPCHPKAPEPCHPKAPEPCHPKAPEPCHPKAPEPCHPKVPEP 120

Qy        112 CHPKAPEPCHPVVPEPCPSTVTPSPYQQKTKQK 144
              | ||||||| |:||||||||||   |||||||
Db        121 CLPKAPEPCQPIVPEPCPSTVTPILAQQKTKQK 153


RESULT 3
US-09-735-705-114
; Sequence 114, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Hosken, Nancy
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Fanger, Neil
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.455C14
;  CURRENT APPLICATION NUMBER: US/09/735,705
;  CURRENT FILING DATE:  2000-12-12
;  NUMBER OF SEQ ID NOS:  419
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 114
;   LENGTH: 161
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-735-705-114

  Query Match           48.2%;  Score 424.5;  DB 3;  Length 161;
  Best Local Similarity  57.8%;  Pred. No. 1.5e-23;
  Matches   93;  Conservative    6;  Mismatches   45;  Indels   17;  Gaps    3;

Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCH-PVPEPCNPKGPEPCHPK 59
              |||:|||| | |||| ||||||| |||||| | ||:|||  ||:| | | |||   |
Db          1 MSSYQQKQTFTPPPQLQQQQVKQPSQPPPQEIFVPTTKEPCHSKVPQPGNTKIPEPGCTK 60

Qy         60 APEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEP----------CQP 106
              |||   | |||  |||||  |||||  |||||  |||||                :|
Db         61 VPEPGCTKVPEPGCTKVPEPGCTKVPEPGCTKVPEPGYTKVPEPGSIKVPDQGFIKFPEP 120

Qy        107 ---KAPEPCHPKAPEPCHPVVPEPCPSTVTPSPYQQKTKQK 144
                  | ||  : | | | :  |||||||||| | |||||||
Db        121 GAIKVPEQGYTKVPVPGYTKVPEPCPSTVTPGPAQQKTKQK 161


RESULT 4
US-09-850-716A-114
; Sequence 114, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
;  APPLICANT: Kalos, Michael D.
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Retter, Marc W.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C15
;  CURRENT APPLICATION NUMBER: US/09/850,716A
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 440
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 114
;   LENGTH: 161
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-850-716A-114

  Query Match           48.2%;  Score 424.5;  DB 3;  Length 161;
  Best Local Similarity  57.8%;  Pred. No. 1.5e-23;
  Matches   93;  Conservative    6;  Mismatches   45;  Indels   17;  Gaps    3;

Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCH-PVPEPCNPKGPEPCHPK 59
              |||:|||| | |||| ||||||| |||||| | ||:|||  ||:| | | |||   |
Db          1 MSSYQQKQTFTPPPQLQQQQVKQPSQPPPQEIFVPTTKEPCHSKVPQPGNTKIPEPGCTK 60

Qy         60 APEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEP----------CQP 106
              |||   | |||  |||||  |||||  |||||  |||||                :|
Db         61 VPEPGCTKVPEPGCTKVPEPGCTKVPEPGCTKVPEPGYTKVPEPGSIKVPDQGFIKFPEP 120

Qy        107 ---KAPEPCHPKAPEPCHPVVPEPCPSTVTPSPYQQKTKQK 144
                  | ||  : | | | :  |||||||||| | |||||||
Db        121 GAIKVPEQGYTKVPVPGYTKVPEPCPSTVTPGPAQQKTKQK 161


RESULT 5
US-09-897-778-114
; Sequence 114, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Marnerakis, Margarita
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Peckham, David W.
;  APPLICANT:  Fanger, Neil
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C16
;  CURRENT APPLICATION NUMBER: US/09/897,778
;  CURRENT FILING DATE:  2001-06-28
;  NUMBER OF SEQ ID NOS: 467
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 114
;   LENGTH: 161
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-897-778-114

  Query Match           48.2%;  Score 424.5;  DB 3;  Length 161;
  Best Local Similarity  57.8%;  Pred. No. 1.5e-23;
  Matches   93;  Conservative    6;  Mismatches   45;  Indels   17;  Gaps    3;
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 12:00:07 ; Search time 235.714 Seconds
(without alignments)
268.420 Million cell updates/sec

Title: US-10-681-398A-2
Perfect score: 880
Sequence: 1 MSSHQQKQPCTVPPQLHQQQ.....PEPCPSTVTPSPYQQKTKQK 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	880	100.0	144	6	ABB98373	Abb98373 Mouse SPR
2	775	88.1	152	7	ADE59751	Ade59751 Rat Prote
3	775	88.1	152	7	ADD45684	Add45684 Rat Prote
4	712.5	81.0	153	8	ADJ76335	Adj76335 Marker ge
5	712.5	81.0	153	8	ADS85103	Ads85103 Mouse ato
6	424.5	48.2	89	8	ABM80143	Abm80143 Tumour-as
7	424.5	48.2	161	2	AAY41031	Aay41031 Human lun
8	424.5	48.2	161	3	AAB11316	Aab11316 Human lun
9	424.5	48.2	161	5	ABB74948	Abb74948 Human lun
10	424.5	48.2	161	5	ABP61868	Abp61868 Human lun
11	424.5	48.2	161	7	ADA28204	Ada28204 Human lun
12	424.5	48.2	161	7	ADE53409	Ade53409 Human lun
13	424.5	48.2	161	7	ADH36768	Adh36768 Human lun
14	424.5	48.2	161	8	ADM56571	Adm56571 Human lun
15	424.5	48.2	161	8	ADN89615	Adn89615 Human lun
16	424.5	48.2	161	9	ADU98263	Adu98263 Lung tumo
17	424.5	48.2	161	9	AEB10071	Aeb10071 Cancer re
18	423.5	48.1	169	6	ABU56429	Abu56429 Lung canc
19	423.5	48.1	169	8	ADN05470	Adn05470 Antipsori
20	421.5	47.9	161	8	ADK70538	Adk70538 Respirato
21	418.5	47.6	89	8	ADK70540	Adk70540 Respirato
22	417.5	47.4	89	6	ABU56433	Abu56433 Lung canc
23	417.5	47.4	89	6	ABU07470	Abu07470 Protein d
24	417.5	47.4	89	8	ADJ75620	Adj75620 Marker ge
25	417.5	47.4	89	8	ADN04108	Adn04108 Antipsori
26	414.5	47.1	89	6	ABU56430	Abu56430 Lung canc
27	414.5	47.1	89	6	ABU56589	Abu56589 Lung canc
28	414.5	47.1	89	8	ADK70542	Adk70542 Respirato
29	414.5	47.1	89	8	ADN04648	Adn04648 Antipsori
30	414.5	47.1	89	8	ADN04682	Adn04682 Antipsori
31	386.5	43.9	89	9	AEA20007	Aea20007 Novel hum
32	246	28.0	513	4	ABU53254	Abu53254 Human tes
33	246	28.0	1270	8	ADK67911	Adk67911 Human ext
34	246	28.0	1299	4	AAM24322	Aam24322 Human EST
35	246	28.0	1311	8	ADK67912	Adk67912 Human ext
36	246	28.0	1320	7	ADK65819	Adk65819 Angiogene
37	246	28.0	1404	2	AAR26049	Aar26049 MSF precu
38	246	28.0	1404	4	AAB29773	Aab29773 Human meg
39	246	28.0	1404	4	AAB60568	Aab60568 Human meg
40	246	28.0	1404	7	ADK65839	Adk65839 Angiogene
41	246	28.0	1404	8	ADM98014	Adm98014 Human meg
42	246	28.0	1404	9	ADX69335	Adx69335 Human hep
43	246	28.0	1404	9	ADY15658	Ady15658 PRO polyp
44	246	28.0	1415	4	AAU32262	Aau32262 Novel hum
45	227.5	25.9	546	4	ABU53252	Abu53252 Human tes

ALIGNMENTS

RESULT 1
ABB98373
ID ABB98373 standard; protein; 144 AA.
XX
AC ABB98373;
XX
DT 04-FEB-2003 (first entry)
XX
DE Mouse SPRR1A SEQ ID NO 2.
XX
KW Mouse; SPRR1A; neuron; neuroprotective; nerve growth; nerve regeneration;
KW peripheral nervous system; PNS; central nervous system; CNS.
XX
OS Mus musculus.
XX
PN WO200285116-A1.
XX
PD 31-OCT-2002.
XX
PF 22-APR-2002; 2002WO-US012564.
XX
PR 21-APR-2001; 2001US-0285373P.
XX
PA (UYYA) UNIV YALE.
XX
PI Strittmatter SM, Bonilla IE;
XX
DR WPI; 2003-093050/08.
DR N-PSDB; ABV99638.
XX
PT Inducing growth of a neuron such as peripheral nervous system neuron or a
PT central nervous system neuron of a mammal, by administering to the neuron
PT SPRR1A polypeptide or its fragment.
XX
PS Claim 2; Page 70-71; 72pp; English.
XX
CC The invention relates to inducing growth of a neuron, comprising
CC administering to the neuron SPRR1A polypeptide (ABB98373) encoded by a
CC nucleic acid comprising a 436 nucleotide sequence (ABV99638) or a SPRR1A
CC peptide (ABB98374). The SPRR1A polypeptide has neuroprotective activity
CC and acts as an inducer of nerve growth and regeneration. The method is
CC useful for inducing growth of a neuron such as a peripheral nervous
CC system neuron or a central nervous system neuron of a mammal, preferably
CC human. The method is also useful for inducing nerve regeneration of a
CC damaged nerve, especially a sciatic nerve
XX
SQ Sequence 144 AA;

```
  Query Match             100.0%;  Score 880;  DB 6;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-59;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCHPVPEPCNPKGPEPCHPKA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCHPVPEPCNPKGPEPCHPKA 60

Qy         61 PEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEPCQPKAPEPCHPKAPEPC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEPCQPKAPEPCHPKAPEPC 120

Qy        121 HPVVPEPCPSTVTPSPYQQKTKQK 144
              ||||||||||||||||||||||||
Db        121 HPVVPEPCPSTVTPSPYQQKTKQK 144


RESULT 2
ADE59751
ID   ADE59751 standard; protein; 152 AA.
XX
AC   ADE59751;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Rat Protein Q63532, SEQ ID NO 5647.
XX
KW   Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW   chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS   Rattus norvegicus.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; Q63532.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a rat protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 152 AA;

  Query Match             88.1%;  Score 775;  DB 7;  Length 152;
  Best Local Similarity   84.2%;  Pred. No. 5.5e-51;
  Matches  128;  Conservative    3;  Mismatches   13;  Indels    8;  Gaps    1;

Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCHPVPEPCNPKGPEPCHPKA 60
              ||| |||||||||||||| :||||||||||||||||:||||:||||||| |||| ||
Db          1 MSSQQQKQPCTVPPQLHQHEVKQPCQPPPQEPCAPKTKEPCHPIPEPCNPKVPEPCQPKV 60

Qy         61 PEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEPCQPKAPEPCH------- 113
              |||| || |||| ||||||||||||||||||||||| ||||||| ||||||||
Db         61 PEPCQPKVPEPCQPKVPEPCQPKVPEPCQPKVPEPCQPKVPEPCHPKAPEPCHPVVPEPC 120

Qy        114 -PKAPEPCHPVVPEPCPSTVTPSPYQQKTKQK 144
               | ||||| |||||||| ||||||||||||||
Db        121 QPVAPEPCQPVVPEPCPPTVTPSPYQQKTKQK 152


RESULT 3
ADD45684
ID   ADD45684 standard; protein; 152 AA.
XX
AC   ADD45684;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Rat Protein Q63532, SEQ ID NO 11352.
XX
KW   Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW   chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS   Rattus norvegicus.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; Q63532.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Claim 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 6, 2006, 12:05:22 ; Search time 41.1429 Seconds
(without alignments)
336.759 Million cell updates/sec

Title: US-10-681-398A-2
Perfect score: 880
Sequence: 1 MSSHQQKQPCTVPPQLHQQQ.....PEPCPSTVTPSPYQQKTKQK 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	616	70.0	126	2	A46375	cornifin - rabbit
2	466.5	53.0	97	2	I51926	small proline-rich
3	418.5	47.6	89	2	A46709	small proline-rich
4	414.5	47.1	89	2	I54187	small proline-rich
5	243	27.6	402	2	A40678	T-cell adhesion re
6	236.5	26.9	544	2	T17547	proline-rich prote
7	213	24.2	1006	2	G86292	hypothetical prote
8	211.5	24.0	439	2	S51939	chitinase (EC 3.2.
9	211.5	24.0	534	2	S21961	proline-rich prote
10	209.5	23.8	207	2	A40215	TcD antigen - Tryp
11	207	23.5	306	2	T52340	cell wall-plasma m
12	202.5	23.0	334	2	A48151	sperm tail protein
13	202.5	23.0	489	2	T11622	extensin class 1 p
14	199	22.6	449	2	S16748	proline-rich prote
15	198.5	22.6	368	2	C29356	hydroxyproline-ric
16	198.5	22.6	1137	2	A86335	T20H2.9 protein -
17	198	22.5	826	2	A45559	sporozoite surface
18	194.5	22.1	242	2	S54156	extensin-like prot
19	193	21.9	72	2	I68511	small proline-rich
20	190	21.6	280	2	T11671	extensin-like prot
21	190	21.6	347	2	T05737	probable hordein C
22	189.5	21.5	376	2	S71558	probable cell wall
23	189.5	21.5	666	2	B70803	hypothetical prote
24	189	21.5	428	2	E71415	probable coll wall
25	188	21.4	72	2	B27725	small proline-rich
26	188	21.4	267	2	S08314	cell wall glycopro
27	188	21.4	332	1	OZZQMB	circumsporozoite p
28	187	21.2	310	2	T06211	C-hordein precurso
29	186.5	21.2	260	2	S18350	seed storage prote
30	186	21.1	181	2	S14974	extensin class I (
31	186	21.1	357	2	S18236	omega secalin prec
32	185.5	21.1	599	2	T10798	pherophorin-S - Vo
33	185	21.0	72	2	S12712	small proline-rich
34	185	21.0	197	2	T10081	sperm mitochondria
35	185	21.0	491	2	T07598	proline-rich prote
36	184.5	21.0	117	2	S24023	dopamine receptor
37	184	20.9	357	2	S18235	omega secalin prec
38	183	20.8	328	2	JQ0985	hydroxyproline-ric
39	183	20.8	496	2	T17908	proline/lysine-ric
40	182.5	20.7	117	2	S24194	dopamine receptor
41	182.5	20.7	303	2	S28264	hydroxyproline-ric
42	182.5	20.7	359	2	B86409	F3H9.6 protein - A
43	182	20.7	348	1	OZZQBK	circumsporozoite p
44	181.5	20.6	839	2	F75518	hypothetical prote
45	181	20.6	388	2	S25298	extensin (clone To

ALIGNMENTS

RESULT 1
A46375
cornifin - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46375
R;Marvin, K.W.; George, M.D.; Fujimoto, W.; Saunders, N.A.; Bernacki, S.H.; Jetten, A.M
Proc. Natl. Acad. Sci. U.S.A. 89, 11026-11030, 1992
A;Title: Cornifin, a cross-linked envelope precursor in keratinocytes that is down-regu
A;Reference number: A46375; MUID:93066377; PMID:1438308
A;Accession: A46375
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-126 <MAR>
A;Cross-references: UNIPROT:P35324; UNIPARC:UPI0000127F17
A;Experimental source: squamous cell
A;Note: sequence extracted from NCBI backbone (NCBIN:118804, NCBIP:118807)
C;Superfamily: hydroxyproline-rich glycoprotein

Query Match 70.0%; Score 616; DB 2; Length 126;
Best Local Similarity 72.2%; Pred. No. 2.3e-36;
Matches 104; Conservative 4; Mismatches 18; Indels 18; Gaps 2;

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Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCHPVPEPCNPKGPEPCHPKA 60
              ||| |||||||:|||| | ||||||||||||||| ||||       ||| || |||| ||
Db          1 MSSQQQKQPCTLPPQLQQHQVKQPCQPPPQEPCVPKTK-------EPCQPKVPEPCQPKV 53

Qy         61 PEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEPCQPKAPEPCHPKAPEPC 120
              |||| || |||| ||||:|||||||||||||||| |||||||||| |||| | |:||
Db         54 PEPCQPKVPEPCQPKVPQPCQPKVPEPCQPKVPEPCQPKVPEPCQPKVPEPCQSKVPQPC 113

Qy        121 HPVVPEPCPSTVTPSPYQQKTKQK 144
               | |||||          :||||
Db        114 QPKVPEPC----------QTKQK 126
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RESULT 2
I51926
small proline-rich protein - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I51926
R;Tesfaigzi, J.; Wright, P.S.; Oreffo, V.; An, G.; Wu, R.; Carlson, D.M.
Am. J. Respir. Cell Mol. Biol. 9, 434-440, 1993
A;Title: A small proline-rich protein regulated by vitamin A in tracheal epithelial cel
A;Reference number: I51926; MUID:94000868; PMID:8398182
A;Accession: I51926
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-97 <TES>
A;Cross-references: UNIPROT:P35323; UNIPARC:UPI0000127F23; GB:M88166; NID:g385239; PIDN
C;Genetics:

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A;Gene: sPRP
C;Superfamily: hydroxyproline-rich glycoprotein

  Query Match           53.0%;  Score 466.5;  DB 2;  Length 97;
  Best Local Similarity   59.7%;  Pred. No. 3.7e-26;
  Matches   86;  Conservative    3;  Mismatches    8;  Indels   47;  Gaps    2;

Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCHPVPEPCNPKGPEPCHPKA 60
              ||| ||||||| ||| |||||||||||||||| ||||:|||
Db          1 MSSQQQKQPCTPPPQPQQQQVKQPCQPPPQEPCVPKTKEPCH------------------ 42

Qy         61 PEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEPCQPKAPEPCHPKAPEPC 120
                          ||||||||||||||||||||||:||||||||||
Db         43 -------------PKVPEPCQPKVPEPCQPKVPEPCHPKVPEPCQPK------------- 76

Qy        121 HPVVPEPCPSTVTPSPYQQKTKQK 144
                 ||||||| | |:| |||||||
Db         77 ---VPEPCPSPVIPAPAQQKTKQK 97


RESULT 3
A46709
small proline-rich protein spr1 - human
N;Alternate names: keratin, small proline rich protein I
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: A46709; A27725
R;An, G.; Tesfaigzi, J.; Chuu, Y.J.; Wu, R.
J. Biol. Chem. 268, 10977-10982, 1993
A;Title: Isolation and characterization of the human spr1 gene and its regulation of exp
A;Reference number: A46709; MUID:93266543; PMID:8388378
A;Accession: A46709
A;Molecule type: DNA
A;Residues: 1-89 <AN1>
A;Cross-references: UNIPROT:P22528; UNIPARC:UPI0000127F1B; GB:M84757; NID:g338433; PIDN:
A;Note: sequence modified after extraction from NCBI backbone
A;Note: the authors translated the codon TGC for residue 65 as Lys
A;Note: sequence extracted from NCBI backbone (NCBIN:132797)
R;Kartasova, T.; van de Putte, P.
Mol. Cell. Biol. 8, 2195-2203, 1988
A;Title: Isolation, characterization, and UV-stimulated expression of two families of ge
A;Reference number: A93100; MUID:88261298; PMID:3133554
A;Accession: A27725
A;Molecule type: mRNA
A;Residues: 1-89 <KAR>
A;Cross-references: UNIPARC:UPI0000127F1B; GB:M19888; NID:g338416; PIDN:AAA36636.1; PID:
C;Superfamily: hydroxyproline-rich glycoprotein

  Query Match           47.6%;  Score 418.5;  DB 2;  Length 89;
  Best Local Similarity   54.2%;  Pred. No. 7.1e-23;
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Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCHPVPEPCNPKGPEPCHPKA 60
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Db          1 MSSQQQKQPCIPPPQLQQQQVKQPCQPPPQEPCIPKTKEPCH------------------ 42

Qy         61 PEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEPCQPKAPEPCHPKAPEPC 120
                                     |||||||:|||||||||| |||||||
Db         43 ----------------------------PKVPEPCHPKVPEPCQPKVPEPCHPK----- 68

Qy        121 HPVVPEPCPSTVTPSPYQQKTKQK 144
                 ||||||| |||:| |||||||
Db         69 ---VPEPCPSIVTPAPAQQKTKQK 89


RESULT 4
I54187
small proline-rich protein 1A - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I54187
R;Gibbs, S.; Fijneman, R.; Wiegant, J.; van Kessel, A.G.; van De Putte, P.; Backendorf,
Genomics 16, 630-637, 1993
A;Title: Molecular characterization and evolution of the SPRR family of keratinocyte d:
A;Reference number: I54187; MUID:93315153; PMID:8325635
A;Accession: I54187
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-89 <RES>
A;Cross-references: UNIPROT:P35321; UNIPARC:UPI0000127F15; GB:L05187; NID:g3327379; PII
C;Genetics:
A;Gene: GDB:SPRR1A
A;Cross-references: GDB:136393; OMIM:182265
A;Map position: 1q21-1q21
C;Superfamily: hydroxyproline-rich glycoprotein

  Query Match           47.1%;  Score 414.5;  DB 2;  Length 89;
  Best Local Similarity   54.2%;  Pred. No. 1.3e-22;
  Matches   78;  Conservative    3;  Mismatches    8;  Indels   55;  Gaps    2;

Qy          1 MSSHQQKQPCTVPPQLHQQQVKQPCQPPPQEPCAPKTKDPCHPVPEPCNPKGPEPCHPKA 60
              |:| ||||||| |||  |||||||||||||||| ||||
Db          1 MNSQQQKQPCTPPPQPQQQQVKQPCQPPPQEPCIPKTK---------------------- 38

Qy         61 PEPCHPKAPEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEPCQPKAPEPCHPKAPEPC 120
                                ||||||||||| ||||||| ||:|||||||
Db         39 -----------------EPCQPKVPEPCHPKVPEPCQPKIPEPCQPK------------- 68

Qy        121 HPVVPEPCPSTVTPSPYQQKTKQK 144
                 ||||||||||:| |||||||
Db         69 ---VPEPCPSTVTPAPAQQKTKQK 89


RESULT 5
A40678
T-cell adhesion receptor CD2 homolog - African swine fever virus
C;Species: African swine fever virus, ASFV
C;Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A40678
R;Rodriguez, J.M.; Yanez, R.J.; Almazan, F.; Vinuela, E.; Rodriguez, J.F.
J. Virol. 67, 5312-5320, 1993
A;Title: African swine fever virus encodes a CD2 homolog responsible for the adhesion c
A;Reference number: A40678; MUID:93353606; PMID:8102411
A;Contents: BA71V
A;Accession: A40678
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-402 <ROD>
A;Cross-references: UNIPROT:Q89501; UNIPARC:UPI00000ED9E7
A;Note: sequence extracted from NCBI backbone (NCBIP:136284)

  Query Match           27.6%;  Score 243;  DB 2;  Length 402;
  Best Local Similarity   41.9%;  Pred. No. 2.9e-10;
  Matches   54;  Conservative   18;  Mismatches   19;  Indels   38;  Gaps   12;

Qy         26 QPPPQEPCAPK----------------TKDPCH--PVPEPCNPKGPEPCHPKAPEPCHPK 67
              :| |:||  ||                :  | :  |:|:|| |  |:|| |  |:|| |
Db        264 EPSPREPLLPKPYSRYQYNTPIYYMRPSTQPLNPFPLPKPCPP--PKPCPP--PKPCPP- 318

Qy         68 APEPCNPKVPEPCQPKVPEPCQPKVPEPCNPKVPEPCQPKAPEPCHPKAPEPCHPVVPEP 127
               |:|| |  |:|| |  |:||:|  |:|| |  |:|| |  |:|| |  |:|| |   :|
Db        319 -PKPCPP--PKPCSP--PKPCRP--PKPCPP--PKPCPP--PKPCPP--PKPCPP--SKP 363

Qy        128 CPSTVTPSP 136
                ||| :. ||
Db        364 CPSPESYSP 372


RESULT 6
T17547
proline-rich protein A57R - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17547
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 6, 2006, 12:37:10 ; Search time 145 Seconds
(without alignments)
5344.944 Million cell updates/sec

Title: US-10-681-398A-1
Perfect score: 436
Sequence: 1 atgagttcccaccagcagaa.....gaagacaaagcagaagtaat 436

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
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9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	169.2	38.8	957	3	US-09-123-912-113	Sequence 113, App
2	169.2	38.8	957	3	US-09-643-597-113	Sequence 113, App
3	169.2	38.8	957	3	US-09-480-884A-113	Sequence 113, App
4	169.2	38.8	957	3	US-09-542-615A-113	Sequence 113, App
5	169.2	38.8	957	3	US-09-606-421B-113	Sequence 113, App
6	169.2	38.8	957	3	US-09-221-107-113	Sequence 113, App
7	169.2	38.8	957	3	US-09-466-396A-113	Sequence 113, App
8	169.2	38.8	957	3	US-09-476-496A-113	Sequence 113, App
9	169.2	38.8	957	3	US-09-630-940B-113	Sequence 113, App
10	169.2	38.8	957	3	US-09-285-479-113	Sequence 113, App
11	169.2	38.8	957	3	US-10-007-700-113	Sequence 113, App
12	156.6	35.9	441	3	US-09-123-912-97	Sequence 97, Appl
13	156.6	35.9	441	3	US-09-643-597-97	Sequence 97, Appl
14	156.6	35.9	441	3	US-09-480-884A-97	Sequence 97, Appl
15	156.6	35.9	441	3	US-09-542-615A-97	Sequence 97, Appl
16	156.6	35.9	441	3	US-09-606-421B-97	Sequence 97, Appl
17	156.6	35.9	441	3	US-09-221-107-97	Sequence 97, Appl
18	156.6	35.9	441	3	US-09-466-396A-97	Sequence 97, Appl
19	156.6	35.9	441	3	US-09-476-496A-97	Sequence 97, Appl
20	156.6	35.9	441	3	US-09-630-940B-97	Sequence 97, Appl
21	156.6	35.9	441	3	US-09-285-479-97	Sequence 97, Appl
22	156.6	35.9	441	3	US-10-007-700-97	Sequence 97, Appl
23	156.6	35.9	600	3	US-09-123-912-98	Sequence 98, Appl
24	156.6	35.9	600	3	US-09-643-597-98	Sequence 98, Appl
25	156.6	35.9	600	3	US-09-480-884A-98	Sequence 98, Appl
26	156.6	35.9	600	3	US-09-542-615A-98	Sequence 98, Appl
27	156.6	35.9	600	3	US-09-606-421B-98	Sequence 98, Appl
28	156.6	35.9	600	3	US-09-221-107-98	Sequence 98, Appl
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30	156.6	35.9	600	3	US-09-476-496A-98	Sequence 98, Appl
31	156.6	35.9	600	3	US-09-630-940B-98	Sequence 98, Appl
32	156.6	35.9	600	3	US-09-285-479-98	Sequence 98, Appl
33	156.6	35.9	600	3	US-10-007-700-98	Sequence 98, Appl
34	153.2	35.1	336	3	US-09-949-016-2217	Sequence 2217, Ap
35	153.2	35.1	601	3	US-09-949-016-33707	Sequence 33707, A
36	153.2	35.1	601	3	US-09-949-016-76311	Sequence 76311, A
37	153.2	35.1	4270	3	US-09-949-016-12549	Sequence 12549, A
38	153.2	35.1	4336	3	US-09-949-016-13959	Sequence 13959, A
39	150	34.4	270	3	US-09-949-016-807	Sequence 807, App
40	117	26.8	1405	3	US-09-244-111-9	Sequence 9, Appli
41	115.2	26.4	470	3	US-09-123-912-95	Sequence 95, Appl
42	115.2	26.4	470	3	US-09-643-597-95	Sequence 95, Appl
43	115.2	26.4	470	3	US-09-480-884A-95	Sequence 95, Appl
44	115.2	26.4	470	3	US-09-542-615A-95	Sequence 95, Appl
45	115.2	26.4	470	3	US-09-606-421B-95	Sequence 95, Appl

ALIGNMENTS

RESULT 1
US-09-123-912-113
; Sequence 113, Application US/09123912A
; Patent No. 6312695
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
; FILE REFERENCE: 210121.455C1
; CURRENT APPLICATION NUMBER: US/09/123,912A
; CURRENT FILING DATE: 1998-07-27
; PRIOR APPLICATION NUMBER: 09/040,802
; PRIOR FILING DATE: 1998-03-18
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
; LENGTH: 957
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-123-912-113

Query Match 38.8%; Score 169.2; DB 3; Length 957;
Best Local Similarity 63.7%; Pred. No. 1.9e-34;
Matches 274; Conservative 0; Mismatches 153; Indels 3; Gaps 1;

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Qy          1 ATGAGTTCCCACCAGCAGAAGCAGCCCTGCACTGTACCTCCTCAGCTGCACCAGCAGCAG 60
              ||||||||  |||||||||||||||| |||  ||   ||| |||||||| || |||||||||
Db        126 ATGAGTTCTTACCAGCAGAAGCAGACCTTTACCCCACCACCTCAGCTTCAACAGCAGCAG 185

Qy         61 GTGAAGCAGCCTTGCCAGCCACCACCCCAGGAACCTTGTGCCCCCAAAACCAAGGATCCC 120
              ||||| || ||  ||||||| ||||| ||||||   | ||  |||| ||||||||| ||
Db        186 GTGAAACAACCCAGCCAGCCTCCACCTCAGGAAATATTTGTTCCCACAACCAAGGAGCCA 245

Qy        121 TGCCACCC---TGTTCCTGAGCCCTGCAACCCCAAGGGGCCAGAGCCCTGCCACCCCAAG 177
              ||||||  |    |||||  | ||  | ||| | |||   ||||||||  ||    |||||
Db        246 TGCCACTCAAAGGTTCCACAACCTGGAAACACAAAGATTCCAGAGCCAGGCTGTACCAAG 305

Qy        178 GCACCCGAGCCCTGCCACCCCAAGGCACCTGAGCCCTGCAACCCCAAGGTGCCAGAGCCC 237
              |  || ||||||  ||     ||||||  ||||||||  |     ||||||| || |||||
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Qy        238 TGCCAGCCTAAGGTGCCAGAGCCCTGCCAGCCTAAGGTGCCAGAGCCCTGCAACCCCAAG 297
              |     | |||||  || |||||  |     | |||||  || |||||  || ||  |||||
Db        366 GGATGTACCAAGGTCCCTGAGCCAGGTTGTACCAAGGTCCCTGAGCCAGGCTACACCAAG 425

Qy        298 GTGCCAGAGCCCTGCCAACCTAAGGCACCAGAGCCTTGCCACCCCAAGGCGCCTGAGCCC 357
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Db        426 GTCCCTGAGCCAGGCAGCATCAAGGTCCCTGACCAAGGCTTCATCAAGTTTCCTGAGCCA 485

Qy        358 TGCCACCCTGTTGTTCCCGAGCCCTGCCCCTCAACTGTCACTCCATCACCATACCAGCAG 417

Db        486 GGTGCCATCAAAGTTCCTGAGCAAGGATACACCAAAGTTCCTGTGCCAGGCTACACAAAG 545

Qy        418 AAGACAAAGC 427

Db        546 GTACCAGAGC 555


RESULT 2
US-09-643-597-113
; Sequence 113, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Hosken, Nancy
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  McNeill, Patricia D.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.455C11
;  CURRENT APPLICATION NUMBER: US/09/643,597
;  CURRENT FILING DATE:  2000-08-21
;  NUMBER OF SEQ ID NOS:  369
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 113
;   LENGTH: 957
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-643-597-113

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  Best Local Similarity   63.7%;  Pred. No. 1.9e-34;
  Matches  274;  Conservative    0;  Mismatches  153;  Indels    3;  Gaps    1;

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Qy        178 GCACCCGAGCCCTGCCACCCCAAGGCACCTGAGCCCTGCAACCCCAAGGTGCCAGAGCCC 237

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RESULT 3
US-09-480-884A-113
; Sequence 113, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Hosken, Nancy A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C6
;  CURRENT APPLICATION NUMBER: US/09/480,884A
;  CURRENT FILING DATE:  2001-08-27
;  NUMBER OF SEQ ID NOS: 330
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 113
;   LENGTH: 957
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-480-884A-113

  Query Match             38.8%;  Score 169.2;  DB 3;  Length 957;
  Best Local Similarity   63.7%;  Pred. No. 1.9e-34;
  Matches  274;  Conservative    0;  Mismatches  153;  Indels    3;  Gaps    1;

Qy          1 ATGAGTTCCCACCAGCAGAAGCAGCCCTGCACTGTACCTCCTCAGCTGCACCAGCAGCAG 60

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Qy         61 GTGAAGCAGCCTTGCCAGCCACCACCCCAGGAACCTTGTGCCCCCAAAACCAAGGATCCC 120

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; Sequence 113, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Bangur, Chaitanya S.
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 6, 2006, 12:59:25 ; Search time 303 Seconds
(without alignments)
3154.863 Million cell updates/sec

Title: US-10-681-398A-1
Perfect score: 436
Sequence: 1 atgagttcccaccagcagaa.....gaagacaaagcagaagtaat 436

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	331.2	76.0	878	12	US-11-136-527-1931	Sequence 1931, Ap
	2	180.4	41.4	600	12	US-11-136-527-6027	Sequence 6027, Ap
	3	170.8	39.2	984	12	US-11-120-318-2	Sequence 2, Appli
	4	169.2	38.8	957	8	US-10-623-155-113	Sequence 113, App
	5	156.6	35.9	441	8	US-10-623-155-97	Sequence 97, Appl
	6	156.6	35.9	600	8	US-10-623-155-98	Sequence 98, Appl
c	7	129.4	29.7	650	6	US-09-925-065A-38645	Sequence 38645, A
c	8	129.4	29.7	650	6	US-09-925-065A-38646	Sequence 38646, A
c	9	128.2	29.4	650	6	US-09-925-065A-38643	Sequence 38643, A
c	10	128.2	29.4	650	6	US-09-925-065A-38644	Sequence 38644, A
c	11	127.8	29.3	659	6	US-09-925-065A-93117	Sequence 93117, A
	12	115.2	26.4	470	8	US-10-623-155-95	Sequence 95, Appl
	13	113.8	26.1	690	6	US-09-925-065A-93118	Sequence 93118, A
	14	113.8	26.1	690	6	US-09-925-065A-93119	Sequence 93119, A
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	18	85.6	19.6	2824	12	US-11-169-232-13	Sequence 13, Appl
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	20	85.6	19.6	3117	12	US-11-169-232-73	Sequence 73, Appl
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	26	85.6	19.6	3945	12	US-11-169-232-49	Sequence 49, Appl
	27	85.6	19.6	3963	12	US-11-169-232-45	Sequence 45, Appl
	28	85.6	19.6	3963	12	US-11-169-232-59	Sequence 59, Appl
	29	85.6	19.6	4065	12	US-11-169-232-47	Sequence 47, Appl
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c	43	63.2	14.5	1321	6	US-09-925-065A-701748	Sequence 701748,
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ALIGNMENTS

RESULT 1
US-11-136-527-1931
; Sequence 1931, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1931
; LENGTH: 878
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (864)..(864)
; OTHER INFORMATION: n is a, c, g, or t
US-11-136-527-1931

Query Match 76.0%; Score 331.2; DB 12; Length 878;
Best Local Similarity 83.9%; Pred. No. 3.4e-68;
Matches 386; Conservative 8; Mismatches 42; Indels 24; Gaps 1;

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Qy          1 ATGAGTTCCCACCAGCAGAAGCAGCCCTGCACTGTACCTCCTCAGCTGCACCAGCAGCAG 60
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Db         45 ATGAGTTCCCASCAGCAGAAGCAGCCTTGCACTGTACCCCCTCAGCTGCACCAGCASSAG 104

Qy         61 GTGAAGCAGCCTTGCCAGCCACCACCCCAGGAACCTTGTGCCCCCAAAACCAAGGATCCC 120
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Qy        121 TGCCACCCTGTTCCTGAGCCCTGCAACCCCAAGGGGCCAGAGCCCTGCCACCCCAAGGCA 180
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Db        285 CAGCCTAAGGTGCCAGAGCCTTGCCAGCCTAAGGTGCCAGAGCCCTGCCAGCCTAAGGTG 344

Qy        301 CCAGAGCCCTGCCAACCTAAGGCACCAGAGCCTTGCCAC---------------------- 339
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Db        345 CCAGAGCCCTGCCATCCCAAGGCACSTGAGCCCTGCCACCCTGTTGTTCCCGAGCCSTGC 404

Qy        340 ---CCCAAGGCGCCTGAGCCCTGCCACCCTGTTGTTCCCGAGCCCTGCCCCTCAACTGTC 396
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; Sequence 6027, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6027
;   LENGTH: 600
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (586)..(586)
;   OTHER INFORMATION: n is a, c, g, or t
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; Sequence 2, Application US/11120318
; Publication No. US20050266497A1
; GENERAL INFORMATION:
;  APPLICANT: LADENSON, JACK H.
;  APPLICANT:  YOUNG, PAMPEE P.
;  APPLICANT:  MODUR, VIJAY
;  TITLE OF INVENTION: METHOD OF ASSESSING THE RISK OF ATHEROSCLEROSIS
;  FILE REFERENCE: 15060-71
;  CURRENT APPLICATION NUMBER: US/11/120,318
;  CURRENT FILING DATE:  2005-05-02
;  PRIOR APPLICATION NUMBER: 60/567,420
;  PRIOR FILING DATE: 2004-04-30
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
;   LENGTH: 984
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-120-318-2

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; Sequence 113, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
;  APPLICANT: Wang, Tongtong
;  APPLICANT:  Peckham, David W.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.455C20
;  CURRENT APPLICATION NUMBER: US/10/623,155
;  CURRENT FILING DATE:  2003-07-17
;  NUMBER OF SEQ ID NOS: 560
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 113
;   LENGTH: 957
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-623-155-113

  Query Match             38.8%;  Score 169.2;  DB 8;  Length 957;
  Best Local Similarity   63.7%;  Pred. No. 1.7e-30;
  Matches  274;  Conservative    0;  Mismatches  153;  Indels    3;  Gaps    1;
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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Title: US-10-681-398A-1
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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	173.6	39.8	229	7	US-10-430-201-1494	Sequence 1494, Ap
4	173.6	39.8	229	7	US-10-430-201-1495	Sequence 1495, Ap
c 5	170.8	39.2	1232	5	US-10-027-632-123564	Sequence 123564,
c 6	170.8	39.2	1232	5	US-10-027-632-123565	Sequence 123565,
c 7	170.8	39.2	1232	6	US-10-027-632-123564	Sequence 123564,
c 8	170.8	39.2	1232	6	US-10-027-632-123565	Sequence 123565,
9	170.8	39.2	3888	9	US-10-756-149-1804	Sequence 1804, Ap
c 10	170	39.0	583	6	US-10-029-386-10124	Sequence 10124, A
11	169.2	38.8	888	5	US-10-116-802-310	Sequence 310, App
12	169.2	38.8	957	3	US-09-735-705-113	Sequence 113, App
13	169.2	38.8	957	3	US-09-850-716A-113	Sequence 113, App
14	169.2	38.8	957	3	US-09-897-778-113	Sequence 113, App
15	169.2	38.8	957	3	US-09-466-396A-113	Sequence 113, App
16	169.2	38.8	957	5	US-10-007-700-113	Sequence 113, App
17	169.2	38.8	957	6	US-10-117-982-113	Sequence 113, App
18	169.2	38.8	957	6	US-10-313-986-113	Sequence 113, App
19	169.2	38.8	957	8	US-10-775-972-113	Sequence 113, App
20	169.2	38.8	957	9	US-10-922-124-113	Sequence 113, App
21	169.2	38.8	1000	8	US-10-357-930-22677	Sequence 22677, A
22	169.2	38.8	1000	8	US-10-357-930-28522	Sequence 28522, A
23	166	38.1	505	3	US-09-918-995-38041	Sequence 38041, A
24	156.6	35.9	441	3	US-09-735-705-97	Sequence 97, Appl
25	156.6	35.9	441	3	US-09-850-716A-97	Sequence 97, Appl
26	156.6	35.9	441	3	US-09-897-778-97	Sequence 97, Appl
27	156.6	35.9	441	3	US-09-466-396A-97	Sequence 97, Appl
28	156.6	35.9	441	5	US-10-007-700-97	Sequence 97, Appl
29	156.6	35.9	441	6	US-10-117-982-97	Sequence 97, Appl
30	156.6	35.9	441	6	US-10-313-986-97	Sequence 97, Appl
31	156.6	35.9	441	8	US-10-775-972-97	Sequence 97, Appl
32	156.6	35.9	441	9	US-10-922-124-97	Sequence 97, Appl
33	156.6	35.9	600	3	US-09-735-705-98	Sequence 98, Appl
34	156.6	35.9	600	3	US-09-850-716A-98	Sequence 98, Appl
35	156.6	35.9	600	3	US-09-897-778-98	Sequence 98, Appl
36	156.6	35.9	600	3	US-09-466-396A-98	Sequence 98, Appl
37	156.6	35.9	600	5	US-10-007-700-98	Sequence 98, Appl
38	156.6	35.9	600	6	US-10-117-982-98	Sequence 98, Appl
39	156.6	35.9	600	6	US-10-313-986-98	Sequence 98, Appl
40	156.6	35.9	600	8	US-10-775-972-98	Sequence 98, Appl
41	156.6	35.9	600	9	US-10-922-124-98	Sequence 98, Appl
42	156.6	35.9	623	3	US-09-954-456-1843	Sequence 1843, Ap
43	156.6	35.9	623	7	US-10-240-425-1302	Sequence 1302, Ap
44	156.6	35.9	623	9	US-10-843-641A-4870	Sequence 4870, Ap
45	156.6	35.9	869	8	US-10-723-860-5642	Sequence 5642, Ap

ALIGNMENTS

RESULT 1
US-10-681-398A-1
; Sequence 1, Application US/10681398A
; Publication No. US20050054094A1
; GENERAL INFORMATION:
; APPLICANT: Strittmatter, Stephen M.
; APPLICANT: Bonilla, Iris E.
; TITLE OF INVENTION: SPRR1A AND AXONAL REGENERATION
; FILE REFERENCE: 044574-5117
; CURRENT APPLICATION NUMBER: US/10/681,398A
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: US 60/285,373
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: PCT/US02/12564
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-681-398A-1

Query Match 100.0%; Score 436; DB 9; Length 436;
Best Local Similarity 100.0%; Pred. No. 6.6e-111;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAGTTCCCACCAGCAGAAGCAGCCCTGCACTGTACCTCCTCAGCTGCACCAGCAGCAG 60
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Db          1 ATGAGTTCCCACCAGCAGAAGCAGCCCTGCACTGTACCTCCTCAGCTGCACCAGCAGCAG 60

Qy         61 GTGAAGCAGCCTTGCCAGCCACCACCCCAGGAACCTTGTGCCCCCAAAACCAAGGATCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTGAAGCAGCCTTGCCAGCCACCACCCCAGGAACCTTGTGCCCCCAAAACCAAGGATCCC 120

Qy        121 TGCCACCCTGTTCCTGAGCCCTGCAACCCCAAGGGGCCAGAGCCCTGCCACCCCAAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGCCACCCTGTTCCTGAGCCCTGCAACCCCAAGGGGCCAGAGCCCTGCCACCCCAAGGCA 180

Qy        181 CCCGAGCCCTGCCACCCCAAGGCACCTGAGCCCTGCAACCCCAAGGTGCCAGAGCCCTGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCGAGCCCTGCCACCCCAAGGCACCTGAGCCCTGCAACCCCAAGGTGCCAGAGCCCTGC 240

Qy        241 CAGCCTAAGGTGCCAGAGCCCTGCCAGCCTAAGGTGCCAGAGCCCTGCAACCCCAAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGCCTAAGGTGCCAGAGCCCTGCCAGCCTAAGGTGCCAGAGCCCTGCAACCCCAAGGTG 300
```

```
Qy        301 CCAGAGCCCTGCCAACCTAAGGCACCAGAGCCTTGCCACCCCAAGGCGCCTGAGCCCTGC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCAGAGCCCTGCCAACCTAAGGCACCAGAGCCTTGCCACCCCAAGGCGCCTGAGCCCTGC 360

Qy        361 CACCCTGTTGTTCCCGAGCCCTGCCCCTCAACTGTCACTCCATCACCATACCAGCAGAAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CACCCTGTTGTTCCCGAGCCCTGCCCCTCAACTGTCACTCCATCACCATACCAGCAGAAG 420

Qy        421 ACAAAGCAGAAGTAAT 436
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Db        421 ACAAAGCAGAAGTAAT 436


RESULT 2
US-10-631-467-1285
; Sequence 1285, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
;  APPLICANT: Genox Research Inc.
;  TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive p
;  TITLE OF INVENTION:  disease
;  FILE REFERENCE: 3462.1005-000
;  CURRENT APPLICATION NUMBER: US/10/631,467
;  CURRENT FILING DATE:  2003-07-31
;  PRIOR APPLICATION NUMBER: JP 2003-077212
;  PRIOR FILING DATE: 2003-03-20
;  PRIOR APPLICATION NUMBER: JP 2002-229312
;  PRIOR FILING DATE: 2002-08-06
;  NUMBER OF SEQ ID NOS: 2086
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1285
;   LENGTH: 688
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-631-467-1285

  Query Match             62.2%;  Score 271;  DB 9;  Length 688;
  Best Local Similarity   76.9%;  Pred. No. 3.2e-65;
  Matches  356;  Conservative    0;  Mismatches   80;  Indels   27;  Gaps    1;

Qy          1 ATGAGTTCCCACCAGCAGAAGCAGCCCTGCACTGTACCTCCTCAGCTGCACCAGCAGCAG 60
              |||||||| || ||||||||||||||||||| |  ||||| ||| ||||  |||| ||
Db         46 ATGAGTTCACATCAGCAGAAGCAGCCCTGCACAGCTCCTCCACAGTTGCATGAGCAACAA 105

Qy         61 GTGAAGCAGCCTTGCCAGCCACCACCCCAGGAACCTTGTGCCCCCAAAACCAAGGATCCC 120
              ||||| |||||||||||||||||||| |  || || |||| | |  ||  ||||   |||
Db        106 GTGAAACAGCCTTGCCAGCCACCACCTCCTGAGCCATGTGTCTCACAAGTCAAGACACCC 165

Qy        121 TG--------------------------CCACCCTGTTCCTGAGCCCTGCAACCCCAAG 153
              ||                          || |   | |||||||||||||| | ||||||
Db        166 TGTGACACCAAGGTTCCTGAGCCCTGCCACCCCAAGGCTCCTGAGCCCTGCCATCCCAAG 225

Qy        154 GGGCCAGAGCCCTGCCACCCCAAGGCACCCGAGCCCTGCCACCCCAAGGCACCTGAGCCC 213
              |  || ||||||||||||||||||| || |||||||||||||||||||| |||||||||
Db        226 GCTCCTGAGCCCTGCCACCCCAAGGCTCCTGAGCCCTGCCACCCCAAGGCTCCTGAGCCC 285

Qy        214 TGCAACCCCAAGGTGCCAGAGCCCTGCCAGCCTAAGGTGCCAGAGCCCTGCCAGCCTAAG 273
              ||| |||||||||  || |||||||||| || ||||  || || |||||||| || |||
Db        286 TGCCACCCCAAGGCTCCTGAGCCCTGCCACCCCAAGGCTCCTGAACCCTGCCACCCCAAG 345

Qy        274 GTGCCAGAGCCCTGCAACCCCAAGGTGCCAGAGCCCTGCCAACCTAAGGCACCAGAGCCT 333
              |  || ||||||||| |||||||||  || |||||||||| || ||||  || |||||
Db        346 GCTCCTGAGCCCTGCCACCCCAAGGCTCCTGAGCCCTGCCACCCCAAGGTTCCTGAGCCC 405

Qy        334 TGCCACCCCAAGGCGCCTGAGCCCTGCCACCCTGTTGTTCCCGAGCCCTGCCCCTCAACT 393
              ||||  |||||||| |||||||||||||| ||  ||||||| |||||||| |||||||||
Db        406 TGCCTTCCCAAGGCTCCTGAGCCCTGCCAACCCATTGTTCCTGAGCCCTGTCCCTCAACT 465

Qy        394 GTCACTCCATCACCATACCAGCAGAAGACAAAGCAGAAGTAAT 436
              |||||||||  || |  ||| ||||||||||||| ||||| |
Db        466 GTCACTCCAATACTAGCCCAACAGAAGACAAAGCAAAAGTAGT 508


RESULT 3
US-10-430-201-1494
; Sequence 1494, Application US/10430201
; Publication No. US20040162679A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Linheng
;  TITLE OF INVENTION: Method for Predicting Gene Potential and Cell Commitment
;  FILE REFERENCE: 40716 (IP-010)
;  CURRENT APPLICATION NUMBER: US/10/430,201
;  CURRENT FILING DATE:  2003-05-05
;  PRIOR APPLICATION NUMBER: US 60/370,114
;  PRIOR FILING DATE: 2002-05-03
;  NUMBER OF SEQ ID NOS: 4879
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1494
;   LENGTH: 229
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-430-201-1494

  Query Match             39.8%;  Score 173.6;  DB 7;  Length 229;
  Best Local Similarity   85.1%;  Pred. No. 2.7e-38;
  Matches  194;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy        130 GTTCCTGAGCCCTGCAACCCCAAGGGGCCAGAGCCCTGCCACCCCAAGGCACCCGAGCCC 189
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Qy        190 TGCCACCCCAAGGCACCTGAGCCCTGCAACCCCAAGGTGCCAGAGCCCTGCCAGCCTAAG 249
              ||||||||||||| |||||||||||| |||||||||  || |||||||||| || |||
Db         62 TGCCACCCCAAGGCTCCTGAGCCCTGCCACCCCAAGGCTCCTGAGCCCTGCCACCCCAAG 121

Qy        250 GTGCCAGAGCCCTGCCAGCCTAAGGTGCCAGAGCCCTGCAACCCCAAGGTGCCAGAGCCC 309
              |  || |||||||||||| || ||||  || || |||||| |||||||||  || ||||||
Db        122 GCTCCTGAGCCCTGCCACCCCAAGGCTCCTGAACCCTGCCACCCCAAGGCTCCTGAGCCC 181

Qy        310 TGCCAACCTAAGGCACCAGAGCCTTGCCACCCCAAGGCGCCTGAGCCC 357
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Db        182 TGCCACCCCAAGGCTCCTGAGCCCTGCCACCCCAAGGTTCCTGAGCCC 229


RESULT 4
US-10-430-201-1495
; Sequence 1495, Application US/10430201
; Publication No. US20040162679A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Linheng
;  TITLE OF INVENTION: Method for Predicting Gene Potential and Cell Commitment
;  FILE REFERENCE: 40716 (IP-010)
;  CURRENT APPLICATION NUMBER: US/10/430,201
;  CURRENT FILING DATE:  2003-05-05
;  PRIOR APPLICATION NUMBER: US 60/370,114
;  PRIOR FILING DATE: 2002-05-03
;  NUMBER OF SEQ ID NOS: 4879
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1495
;   LENGTH: 229
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-430-201-1495

  Query Match             39.8%;  Score 173.6;  DB 7;  Length 229;
  Best Local Similarity   85.1%;  Pred. No. 2.7e-38;
  Matches  194;  Conservative    0;  Mismatches   34;  Indels    0;  Gaps    0;

Qy        130 GTTCCTGAGCCCTGCAACCCCAAGGGGCCAGAGCCCTGCCACCCCAAGGCACCCGAGCCC 189
              |||||||||||||| |||||||||  || |||||||||| |||||||| || ||||||
Db          2 GTTCCTGAGCCCTGCCACCCCAAGGCTCCTGAGCCCTGCCATCCCAAGGCTCCTGAGCCC 61

Qy        190 TGCCACCCCAAGGCACCTGAGCCCTGCAACCCCAAGGTGCCAGAGCCCTGCCAGCCTAAG 249
              ||||||||||||| |||||||||||| |||||||||  || |||||||||| || |||
Db         62 TGCCACCCCAAGGCTCCTGAGCCCTGCCACCCCAAGGCTCCTGAGCCCTGCCACCCCAAG 121
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 6, 2006, 12:19:48 ; Search time 475 Seconds
(without alignments)
6117.486 Million cell updates/sec

Title: US-10-681-398A-1
Perfect score: 436
Sequence: 1 atgagttcccaccagcagaa.....gaagacaaagcagaagtaat 436

Scoring table: IDENTITY_NUC
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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	436	100.0	436	8	ABV99638	Abv99638 Mouse SPR
2	436	100.0	783	14	ADX26084	Adx26084 Novel cel
3	330	75.7	776	10	ADB57951	Adb57951 Toxicity-
4	271	62.2	688	12	ADJ76033	Adj76033 Marker ge
5	271	62.2	688	13	ADS85102	Ads85102 Mouse ato
6	173.6	39.8	229	12	ADL85102	Adl85102 DNA up-re
7	173.6	39.8	229	12	ADL85101	Adl85101 DNA up-re
8	170.8	39.2	900	13	ACN37461	Acn37461 Tumour-as
9	170.8	39.2	984	8	ABX76147	Abx76147 Lung canc
10	170.8	39.2	984	12	ADN05469	Adn05469 Antipsori
11	170.8	39.2	1065	4	AAH73264	Aah73264 Human cer
c 12	170	39.0	583	12	ACH76929	Ach76929 Human gen
13	169.2	38.8	888	9	ACH04105	Ach04105 Human cDN
14	169.2	38.8	957	3	AAC65850	Aac65850 Human lun
15	169.2	38.8	957	6	ABL49069	Abl49069 Human lun
16	169.2	38.8	957	6	ABQ92255	Abq92255 Human lun
17	169.2	38.8	957	9	ADA28203	Ada28203 Human lun
18	169.2	38.8	957	10	ADE53408	Ade53408 Human lun
19	169.2	38.8	957	10	ADH36767	Adh36767 Human lun
20	169.2	38.8	957	12	ADM56570	Adm56570 Human lun
21	169.2	38.8	957	12	ADN89614	Adn89614 Human lun
22	169.2	38.8	957	14	ADU98262	Adu98262 Lung tumo
23	169.2	38.8	957	14	AEB10070	Aeb10070 Cancer re
24	169.2	38.8	1000	5	ABV22684	Abv22684 Human pro
25	169.2	38.8	1000	5	ABV28509	Abv28509 Human pro
26	169.2	38.8	1014	12	ADK70275	Adk70275 Respirato
27	166	38.1	505	9	ACH50829	Ach50829 Human mam
28	157.4	36.1	955	2	AAZ24611	Aaz24611 Human lun
29	156.6	35.9	441	2	AAZ24597	Aaz24597 Human lun
30	156.6	35.9	441	3	AAC65836	Aac65836 Human lun
31	156.6	35.9	441	6	ABL49055	Abl49055 Human lun
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34	156.6	35.9	441	10	ADE53616	Ade53616 Human lun
35	156.6	35.9	441	10	ADH36751	Adh36751 Human lun
36	156.6	35.9	441	12	ADM56554	Adm56554 Human lun
37	156.6	35.9	441	12	ADN89598	Adn89598 Human lun
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39	156.6	35.9	441	14	AEB10054	Aeb10054 Cancer re
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43	156.6	35.9	600	6	ABQ92242	Abq92242 Human lun
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ALIGNMENTS

RESULT 1
ABV99638
ID ABV99638 standard; cDNA; 436 BP.
XX
AC ABV99638;
XX
DT 04-FEB-2003 (first entry)
XX
DE Mouse SPRR1A encoding cDNA SEQ ID NO 1.
XX
KW Mouse; SPRR1A; neuron; neuroprotective; nerve growth; nerve regeneration;
KW peripheral nervous system; PNS; central nervous system; CNS;
KW GenBank Accession Number X91824; gene; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1. .435
FT /*tag= a
FT /product= "SPRR1A"
XX
PN WO200285116-A1.
XX
PD 31-OCT-2002.
XX
PF 22-APR-2002; 2002WO-US012564.
XX
PR 21-APR-2001; 2001US-0285373P.
XX
PA (UYYA) UNIV YALE.
XX
PI Strittmatter SM, Bonilla IE;
XX
DR WPI; 2003-093050/08.
DR P-PSDB; ABB98373.
XX
PT Inducing growth of a neuron such as peripheral nervous system neuron or a
PT central nervous system neuron of a mammal, by administering to the neuron
PT SPRR1A polypeptide or its fragment.
XX
PS Claim 1; Page 70; 72pp; English.
XX

```
CC   The invention relates to inducing growth of a neuron, comprising
CC   administering to the neuron SPRR1A polypeptide (ABB98373) encoded by a
CC   nucleic acid comprising a 436 nucleotide sequence (ABV99638) or a SPRR1A
CC   peptide (ABB98374). The SPRR1A polypeptide has neuroprotective activity
CC   and acts as an inducer of nerve growth and regeneration. The method is
CC   useful for inducing growth of a neuron such as a peripheral nervous
CC   system neuron or a central nervous system neuron of a mammal, preferably
CC   human. The method is also useful for inducing nerve regeneration of a
CC   damaged nerve, especially a sciatic nerve
XX
SQ   Sequence 436 BP; 104 A; 181 C; 96 G; 55 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 436;  DB 8;  Length 436;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-95;
  Matches  436;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGTTCCCACCAGCAGAAGCAGCCCTGCACTGTACCTCCTCAGCTGCACCAGCAGCAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGAGTTCCCACCAGCAGAAGCAGCCCTGCACTGTACCTCCTCAGCTGCACCAGCAGCAG 60

Qy         61 GTGAAGCAGCCTTGCCAGCCACCACCCCAGGAACCTTGTGCCCCCAAAACCAAGGATCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTGAAGCAGCCTTGCCAGCCACCACCCCAGGAACCTTGTGCCCCCAAAACCAAGGATCCC 120

Qy        121 TGCCACCCTGTTCCTGAGCCCTGCAACCCCAAGGGGCCAGAGCCCTGCCACCCCAAGGCA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TGCCACCCTGTTCCTGAGCCCTGCAACCCCAAGGGGCCAGAGCCCTGCCACCCCAAGGCA 180

Qy        181 CCCGAGCCCTGCCACCCCAAGGCACCTGAGCCCTGCAACCCCAAGGTGCCAGAGCCCTGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCGAGCCCTGCCACCCCAAGGCACCTGAGCCCTGCAACCCCAAGGTGCCAGAGCCCTGC 240

Qy        241 CAGCCTAAGGTGCCAGAGCCCTGCCAGCCTAAGGTGCCAGAGCCCTGCAACCCCAAGGTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGCCTAAGGTGCCAGAGCCCTGCCAGCCTAAGGTGCCAGAGCCCTGCAACCCCAAGGTG 300

Qy        301 CCAGAGCCCTGCCAACCTAAGGCACCAGAGCCTTGCCACCCCAAGGCGCCTGAGCCCTGC 360
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Db        301 CCAGAGCCCTGCCAACCTAAGGCACCAGAGCCTTGCCACCCCAAGGCGCCTGAGCCCTGC 360

Qy        361 CACCCTGTTGTTCCCGAGCCCTGCCCCTCAACTGTCACTCCATCACCATACCAGCAGAAG 420
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Db        361 CACCCTGTTGTTCCCGAGCCCTGCCCCTCAACTGTCACTCCATCACCATACCAGCAGAAG 420

Qy        421 ACAAAGCAGAAGTAAT 436
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Db        421 ACAAAGCAGAAGTAAT 436


RESULT 2
ADX26084
ID   ADX26084 standard; DNA; 783 BP.
XX
AC   ADX26084;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Novel cell pain response detection method-related mouse gene SeqID430.
XX
KW   pain; animal disease model; expression; analgesic; antiaddictive;
KW   nootropic; anticonvulsant; vasotropic; neuroprotective; tranquilizer;
KW   antiasthmatic; antirheumatic; antiarthritic; osteopathic;
KW   ophthalmological; antiinflammatory; antipruritic; dermatological;
KW   antiulcer; gastrointestinal-Gen.; nephrotropic; gynecological;
KW   hepatotropic; antiparkinsonian; neuroleptic; laxative; gene therapy;
KW   neuropathic pain; Alzheimers disease; Parkinsons disease;
KW   motor neurone disease; Huntingtons disease; schizophrenia; gene; ds.
XX
OS   Mus sp.
XX
PN   WO2005014849-A2.
XX
PD   17-FEB-2005.
XX
PF   06-JUL-2004; 2004WO-US023166.
XX
PR   03-JUL-2003; 2003US-0485101P.
XX
PA   (EURO-) EUROCELTIQUE SA.
XX
PI   Tong J,  Jin G,  Ji R,  Xu Y,  Chiang LW,  Lavery DJ;
XX
DR   WPI; 2005-163258/17.
XX
PT   Detecting pain responses in a cell, useful in identifying potential
PT   therapeutic and diagnostic candidates for treating pain, by identifying
PT   genes that are differentially expressed in a model of neuropathic pain.
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PS   Example 1; SEQ ID NO 430; 173pp; English.
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CC   This invention relates to a novel method of detecting a pain response in
CC   a cell which comprises determining the expression level in a test cell of
CC   at least one nucleic acid molecule and comparing the expression level to
CC   a level in an animal model of pain, where similar or identical expression
CC   levels indicate a pain response in the test cell. The invention may be
CC   useful for the development of compounds with an analgesic, antiaddictive,
CC   nootropic, anticonvulsant, vasotropic, neuroprotective, tranquilizer,
CC   antiasthmatic, antirheumatic, antiarthritic, osteopathic,
CC   ophthalmological, antiinflammatory, antipruritic, dermatological,
CC   antiulcer, gastrointestinal-Gen., nephrotropic, gynecological,
CC   hepatotropic, antiparkinsonian, neuroleptic or laxative activity whilst
CC   the disclosed sequences may prove useful for gene therapy. The methods
CC   and compositions of the present invention are useful for identifying
CC   agonists and antagonists for the gene or gene products as potential
CC   therapeutic and diagnostic candidates for treating pain, including
CC   neuropathic pain, nociceptive pain, chronic pain, inflammatory pain, pain
CC   associated with cancer, and pain associated with rheumatic disease, and
CC   also for addiction, seizure, stroke, ischemia, a neurodegenerative
CC   disorder, anxiety, depression, headache, asthma, rheumatic disease,
CC   osteoarthritis, retinopathy, inflammatory eye disorders, pruritus, ulcer,
CC   gastric lesions, uncontrollable urination, an inflammatory or unstable
CC   bladder disorder, inflammatory bowel disease, irritable bowel syndrome
CC   (IBS), irritable bowel disease (IBD), gastroesophageal reflux disease
CC   (GERD), functional dyspepsia, functional chest pain of presumed
CC   esophageal origin, functional dysphagia, non-cardiac chest pain,
CC   symptomatic gastroesophageal disease, gastritis, aerophagia, functional
CC   constipation, functional diarrhea, burbulence, chronic functional
CC   abdominal pain, recurrent abdominal pain (RAP), function abdominal
CC   bloating, functional biliary pain, functional incontinence, functional
CC   ano-rectal disorder, cholecystalgia, interstitial cystitis, dysmenorrhea,
CC   or dyspareunia. They can also be used diagnosing or treating Alzheimer's
CC   disease, Parkinson's disease, amyotrophic lateral sclerosis, Huntington's
CC   disease and schizophrenia. The present sequence is that of a mouse gene
CC   which demonstrated homology to a human gene whose expression level
CC   analysed in the method of the invention.
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SQ   Sequence 783 BP; 186 A; 277 C; 162 G; 158 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 436;  DB 14;  Length 783;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-95;
  Matches  436;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGTTCCCACCAGCAGAAGCAGCCCTGCACTGTACCTCCTCAGCTGCACCAGCAGCAG 60
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Db         46 ATGAGTTCCCACCAGCAGAAGCAGCCCTGCACTGTACCTCCTCAGCTGCACCAGCAGCAG 105

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Db        166 TGCCACCCTGTTCCTGAGCCCTGCAACCCCAAGGGGCCAGAGCCCTGCCACCCCAAGGCA 225

Qy        181 CCCGAGCCCTGCCACCCCAAGGCACCTGAGCCCTGCAACCCCAAGGTGCCAGAGCCCTGC 240
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